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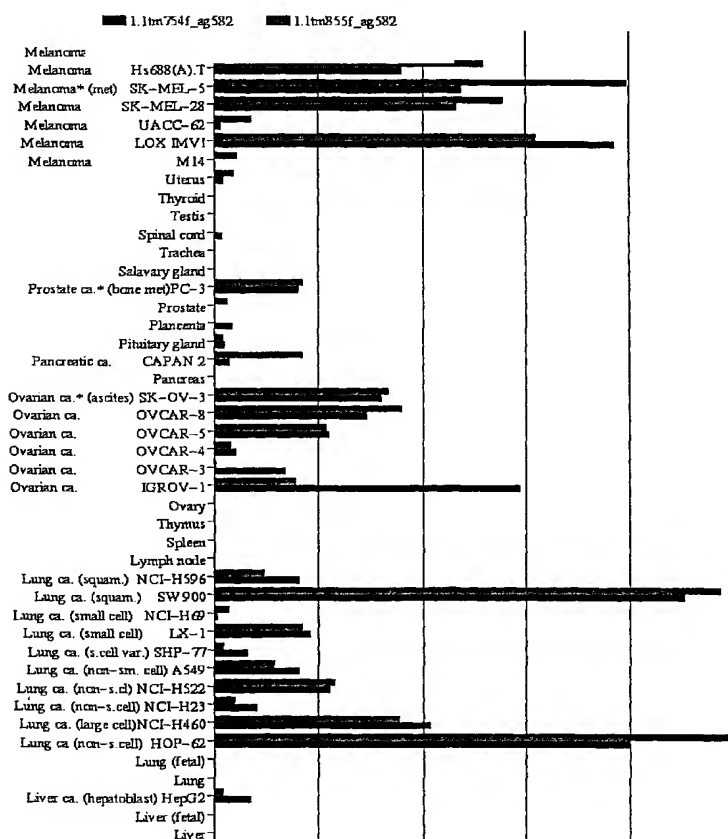
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(54) Title: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME



(57) Abstract: Disclosed herein are nucleic acid sequences that encode novel polypeptides. Also disclosed are polypeptides encoded by these nucleic acid sequences, and antibodies, which immunospecifically-bind to the polypeptide, as well as derivatives, variants, mutants, or fragments of the aforementioned polypeptide, polynucleotide, or antibody. The invention further discloses therapeutic, diagnostic and research methods for diagnosis, treatment, and prevention of disorders involving any one of these novel human nucleic acids and proteins.

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NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME

FIELD OF THE INVENTION

The invention generally relates to nucleic acids and polypeptides encoded therefrom.

BACKGROUND OF THE INVENTION

The invention generally relates to nucleic acids and polypeptides encoded therefrom. More specifically, the invention relates to nucleic acids encoding cytoplasmic, nuclear, membrane bound, and secreted polypeptides, as well as vectors, host cells, antibodies, and recombinant methods for producing these nucleic acids and polypeptides.

SUMMARY OF THE INVENTION

The invention is based in part upon the discovery of nucleic acid sequences encoding novel polypeptides. The novel nucleic acids and polypeptides are referred to herein as NOVX, or NOV1, NOV2, NOV3, NOV4, NOV5, NOV6, NOV7, NOV8, and NOV9 nucleic acids and polypeptides. These nucleic acids and polypeptides, as well as derivatives, homologs, analogs and fragments thereof, will hereinafter be collectively designated as "NOVX" nucleic acid or polypeptide sequences.

In one aspect, the invention provides an isolated NOVX nucleic acid molecule encoding a NOVX polypeptide that includes a nucleic acid sequence that has identity to the nucleic acids disclosed in SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, and 33. In some embodiments, the NOVX nucleic acid molecule will hybridize under stringent conditions to a nucleic acid sequence complementary to a nucleic acid molecule that includes a protein-coding sequence of a NOVX nucleic acid sequence. The invention also includes an isolated nucleic acid that encodes a NOVX polypeptide, or a fragment, homolog, analog or derivative thereof. For example, the nucleic acid can encode a polypeptide at least 80% identical to a polypeptide comprising the amino acid sequences of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, and 34. The nucleic acid can be, for example, a genomic DNA fragment or a cDNA molecule that includes the nucleic acid sequence of any of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, and 33.

Also included in the invention is an oligonucleotide, *e.g.*, an oligonucleotide which includes at least 6 contiguous nucleotides of a NOVX nucleic acid (*e.g.*, SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, and 33) or a complement of said oligonucleotide.

Also included in the invention are substantially purified NOVX polypeptides (SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, and 34). In certain embodiments, the NOVX polypeptides include an amino acid sequence that is substantially identical to the amino acid sequence of a human NOVX polypeptide.

The invention also features antibodies that immunoselectively bind to NOVX polypeptides, or fragments, homologs, analogs or derivatives thereof.

In another aspect, the invention includes pharmaceutical compositions that include therapeutically- or prophylactically-effective amounts of a therapeutic and a pharmaceutically-acceptable carrier. The therapeutic can be, *e.g.*, a NOVX nucleic acid, a NOVX polypeptide, or an antibody specific for a NOVX polypeptide. In a further aspect, the invention includes, in one or more containers, a therapeutically- or prophylactically-effective amount of this pharmaceutical composition.

In a further aspect, the invention includes a method of producing a polypeptide by culturing a cell that includes a NOVX nucleic acid, under conditions allowing for expression of the NOVX polypeptide encoded by the DNA. If desired, the NOVX polypeptide can then be recovered.

In another aspect, the invention includes a method of detecting the presence of a NOVX polypeptide in a sample. In the method, a sample is contacted with a compound that selectively binds to the polypeptide under conditions allowing for formation of a complex between the polypeptide and the compound. The complex is detected, if present, thereby identifying the NOVX polypeptide within the sample.

The invention also includes methods to identify specific cell or tissue types based on their expression of a NOVX.

Also included in the invention is a method of detecting the presence of a NOVX nucleic acid molecule in a sample by contacting the sample with a NOVX nucleic acid probe or primer, and detecting whether the nucleic acid probe or primer bound to a NOVX nucleic acid molecule in the sample.

In a further aspect, the invention provides a method for modulating the activity of a NOVX polypeptide by contacting a cell sample that includes the NOVX polypeptide with a

compound that binds to the NOVX polypeptide in an amount sufficient to modulate the activity of said polypeptide. The compound can be, *e.g.*, a small molecule, such as a nucleic acid, peptide, polypeptide, peptidomimetic, carbohydrate, lipid or other organic (carbon containing) or inorganic molecule, as further described herein.

Also within the scope of the invention is the use of a therapeutic in the manufacture of a medicament for treating or preventing disorders or syndromes including, *e.g.*, diabetes, metabolic disturbances associated with obesity, the metabolic syndrome X, anorexia, wasting disorders associated with chronic diseases, metabolic disorders, diabetes, obesity, infectious disease, anorexia, cancer-associated cachexia, cancer, neurodegenerative disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders, and hematopoietic disorders, or other disorders related to cell signal processing and metabolic pathway modulation. The therapeutic can be, *e.g.*, a NOVX nucleic acid, a NOVX polypeptide, or a NOVX-specific antibody, or biologically-active derivatives or fragments thereof.

For example, the compositions of the present invention will have efficacy for treatment of patients suffering from: developmental diseases, MHCII and III diseases (immune diseases), taste and scent detectability Disorders, Burkitt's lymphoma, corticoneurogenic disease, signal transduction pathway disorders, Retinal diseases including those involving photoreception, Cell growth rate disorders; cell shape disorders, feeding disorders; control of feeding; potential obesity due to over-eating; potential disorders due to starvation (lack of appetite), noninsulin-dependent diabetes mellitus (NIDDM1), bacterial, fungal, protozoal and viral infections (particularly infections caused by HIV-1 or HIV-2), pain, cancer (including but not limited to neoplasm; adenocarcinoma; lymphoma; prostate cancer; uterus cancer), anorexia, bulimia, asthma, Parkinson's disease, acute heart failure, hypotension, hypertension, urinary retention, osteoporosis, Crohn's disease; multiple sclerosis; Albright Hereditary Osteodystrophy, angina pectoris, myocardial infarction, ulcers, asthma, allergies, benign prostatic hypertrophy, and psychotic and neurological disorders, including anxiety, schizophrenia, manic depression, delirium, dementia, severe mental retardation. Dentatorubro-pallidoluysian atrophy (DRPLA) Hypophosphatemic rickets, autosomal dominant (2) Acrocallosal syndrome and dyskinesias, such as Huntington's disease or Gilles de la Tourette syndrome and/or other pathologies and disorders of the like.

The polypeptides can be used as immunogens to produce antibodies specific for the invention, and as vaccines. They can also be used to screen for potential agonist and antagonist

compounds. For example, a cDNA encoding NOVX may be useful in gene therapy, and NOVX may be useful when administered to a subject in need thereof. By way of non-limiting example, the compositions of the present invention will have efficacy for treatment of patients suffering from bacterial, fungal, protozoal and viral infections (particularly infections caused by HIV-1 or HIV-2), pain, cancer (including but not limited to Neoplasm; adenocarcinoma; lymphoma; prostate cancer; uterus cancer), anorexia, bulimia, asthma, Parkinson's disease, acute heart failure, hypotension, hypertension, urinary retention, osteoporosis, Crohn's disease; multiple sclerosis; and Treatment of Albright Hereditary Osteodystrophy, angina pectoris, myocardial infarction, ulcers, asthma, allergies, benign prostatic hypertrophy, and psychotic and neurological disorders, including anxiety, schizophrenia, manic depression, delirium, dementia, severe mental retardation and dyskinesias, such as Huntington's disease or Gilles de la Tourette syndrome and/or other pathologies and disorders.

The invention further includes a method for screening for a modulator of disorders or syndromes including, *e.g.*, diabetes, metabolic disturbances associated with obesity, the metabolic syndrome X, anorexia, wasting disorders associated with chronic diseases, metabolic disorders, diabetes, obesity, infectious disease, anorexia, cancer-associated cachexia, cancer, neurodegenerative disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders, and hematopoietic disorders or other disorders related to cell signal processing and metabolic pathway modulation. The method includes contacting a test compound with a NOVX polypeptide and determining if the test compound binds to said NOVX polypeptide. Binding of the test compound to the NOVX polypeptide indicates the test compound is a modulator of activity, or of latency or predisposition to the aforementioned disorders or syndromes.

Also within the scope of the invention is a method for screening for a modulator of activity, or of latency or predisposition to an disorders or syndromes including, *e.g.*, diabetes, metabolic disturbances associated with obesity, the metabolic syndrome X, anorexia, wasting disorders associated with chronic diseases, metabolic disorders, diabetes, obesity, infectious disease, anorexia, cancer-associated cachexia, cancer, neurodegenerative disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders, and hematopoietic disorders or other disorders related to cell signal processing and metabolic pathway modulation by administering a test compound to a test animal at increased risk for the aforementioned disorders or syndromes. The test animal expresses a recombinant polypeptide encoded by a NOVX nucleic acid. Expression or activity of NOVX polypeptide is then measured in the test animal, as is

expression or activity of the protein in a control animal which recombinantly-expresses NOVX polypeptide and is not at increased risk for the disorder or syndrome. Next, the expression of NOVX polypeptide in both the test animal and the control animal is compared. A change in the activity of NOVX polypeptide in the test animal relative to the control animal indicates the test compound is a modulator of latency of the disorder or syndrome.

In yet another aspect, the invention includes a method for determining the presence of or predisposition to a disease associated with altered levels of a NOVX polypeptide, a NOVX nucleic acid, or both, in a subject (*e.g.*, a human subject). The method includes measuring the amount of the NOVX polypeptide in a test sample from the subject and comparing the amount of the polypeptide in the test sample to the amount of the NOVX polypeptide present in a control sample. An alteration in the level of the NOVX polypeptide in the test sample as compared to the control sample indicates the presence of or predisposition to a disease in the subject. Preferably, the predisposition includes, *e.g.*, diabetes, metabolic disturbances associated with obesity, the metabolic syndrome X, anorexia, wasting disorders associated with chronic diseases, metabolic disorders, diabetes, obesity, infectious disease, anorexia, cancer-associated cachexia, cancer, neurodegenerative disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders, and hematopoietic disorders. Also, the expression levels of the new polypeptides of the invention can be used in a method to screen for various cancers as well as to determine the stage of cancers.

In a further aspect, the invention includes a method of treating or preventing a pathological condition associated with a disorder in a mammal by administering to the subject a NOVX polypeptide, a NOVX nucleic acid, or a NOVX-specific antibody to a subject (*e.g.*, a human subject), in an amount sufficient to alleviate or prevent the pathological condition. In preferred embodiments, the disorder, includes, *e.g.*, diabetes, metabolic disturbances associated with obesity, the metabolic syndrome X, anorexia, wasting disorders associated with chronic diseases, metabolic disorders, diabetes, obesity, infectious disease, anorexia, cancer-associated cachexia, cancer, neurodegenerative disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders, and hematopoietic disorders.

In yet another aspect, the invention can be used in a method to identify the cellular receptors and downstream effectors of the invention by any one of a number of techniques commonly employed in the art. These include but are not limited to the two-hybrid system, affinity purification, co-precipitation with antibodies or other specific-interacting molecules.

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, suitable methods and materials are described below. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. In the case of conflict, the present specification, including definitions, will control. In addition, the materials, methods, and examples are illustrative only and not intended to be limiting.

Other features and advantages of the invention will be apparent from the following detailed description and claims.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1 shows a TaqMan tissue profile result for NOV7.

FIG. 2 shows a replicate TaqMan profiles for NOV7 in a broader range of cancer cells that were derived from surgical specimens.

DETAILED DESCRIPTION OF THE INVENTION

The present invention provides novel nucleotides and polypeptides encoded thereby. Included in the invention are the novel nucleic acid sequences and their polypeptides. The sequences are collectively referred to as "NOVX nucleic acids" or "NOVX polynucleotides" and the corresponding encoded polypeptides are referred to as "NOVX polypeptides" or "NOVX proteins." Unless indicated otherwise, "NOVX" is meant to refer to any of the novel sequences disclosed herein. Table A provides a summary of the NOVX nucleic acids and their encoded polypeptides.

TABLE A. Sequences and Corresponding SEQ ID Numbers

NOVX Assignment	Internal Identification	SEQ ID NO (nucleic acid)	SEQ ID NO (polypeptide)	Homology
1	30235661_EXT1	1	2	TSK-1-like
2a	ba518k17A	3	4	beta Thymosin
2b	518k17_A1	5	6	beta Thymosin
2c	518k17_A	7	8	beta Thymosin
3a	GM_ba63k6_A	9	10	Connexin-like
3b	CG54734-02	11	12	Connexin-like
4a	85731808_EXT	13	14	Hepatoma Derived Growth Factor
4b	21143463.0.45	15	16	Hepatoma Derived Growth Factor
4c	21143463_A.0.45_EXT	17	18	Hepatoma Derived Growth Factor
4d	117477333_EXT	19	20	Hepatoma Derived Growth Factor
5a	21647246_EXT	21	22	Cortexin-like
5b	21647246_da1	21	22	Cortexin-like
6	27926453_EXT1	23	24	Sialoadhesin-like
7	105180778	25	26	Trio Phosphoprotein
8a	3277789_EXT	27	28	Stra6-like
8b	CG52276-03	29	30	Stra6-like
8c	CG52276-04	31	32	Retinoic Acid Responsive-like
9	SC_108341967_A	33	34	Thyroid Regulated Gene

NOVX nucleic acids and their encoded polypeptides are useful in a variety of applications and contexts. The various NOVX nucleic acids and polypeptides according to the invention are useful as novel members of the protein families according to the presence of domains and sequence relatedness to previously described proteins. Additionally, NOVX nucleic acids and polypeptides can also be used to identify proteins that are members of the family to which the NOVX polypeptides belong.

For example, NOV1 is homologous to a testis specific serine/threonine protein kinase (TSK-1) family of proteins that exhibits dual specific protein kinase activity on both serine/threonine and tyrosine and is expressed in testis. Thus, the NOV1 nucleic acids, polypeptides, antibodies and related compounds according to the invention will be useful in therapeutic and diagnostic applications implicated in, for example; Spermatogenesis, Male Reproductive Health, Fertility and/or other pathologies/disorders.

Also, NOV2a, 2b and 2c are homologous to the beta thymosin family of proteins. Thus NOV2 nucleic acids, polypeptides, antibodies and related compounds according to the invention will be useful in therapeutic and diagnostic applications implicated in, for example; prostate cancer, apoptosis, angiogenesis and wound healing, neurodegenerative and neuropsychiatric disease, immune and autoimmune disorders, age-related disorders and/or other pathologies/disorders.

Further, NOV3a and 3b are homologous to a family of connexin-like proteins which are important in forming specialized cell-cell contact sites. Thus, the NOV3 nucleic acids and polypeptides, antibodies and related compounds according to the invention will be useful in therapeutic and diagnostic applications implicated in, for example; Clouston syndrome and deafness, mutilating palmoplantar keratoderma (PPK), X-linked Charcot-Marie-Tooth neuropathy, hereditary peripheral neuropathy and/or other pathologies/disorders.

Also, NOV4a, 4b, 4c and 4d are homologous to the hepatoma derived growth factor family of proteins which are important endothelial cell mitogens. Thus, NOV4 nucleic acids, polypeptides, antibodies and related compounds according to the invention will be useful in therapeutic and diagnostic applications implicated in, for example; Adrenoleukodystrophy, Hemophilia, Hypercoagulation, Immunodeficiencies, Alzheimer's disease, Stroke, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Multiple sclerosis and/or other pathologies/disorders.

Additionally, NOV5a and NOV5b are homologous to the cortexin family of proteins. Thus NOV5 nucleic acids, polypeptides, antibodies and related compounds according to the invention will be useful in treating a variety of conditions, including, *e.g.*, Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, stroke, tuberous sclerosis, hypercalceimia, etc.

Also, NOV6 is homologous to the sialoadhesin-like family of proteins. Thus NOV6 nucleic acids, polypeptides, antibodies and related compounds according to the invention will be useful in therapeutic and diagnostic applications in various disorders, including, for example, involving cell-cell interactions.

Further, NOV7 is homologous to members of the Trio Phosphoprotein family of proteins. Thus, the NOV7 nucleic acids, polypeptides, antibodies and related compounds according to the invention will be useful in therapeutic and diagnostic applications in disorders characterized by, *e.g.*, impaired cell migration and anchorage-independent growth.

Still further, NOV8 is homologous to a family of Stra6-like or retinoic acid responsive-like proteins that are important in a variety of functions. Thus, NOV8 nucleic acids and polypeptides, antibodies and related compounds according to the invention will be useful in therapeutic and diagnostic applications in disorders including, for example, osteoporosis, hypercalceimia, arthritis, ankylosing spondylitis, scoliosis, muscular dystrophy, Lesch-Nyhan syndrome, myasthenia gravis, reproductive disorders, fertility disorders, developmental

disorders, endocrine/growth disorders, disorders in pubertal development, surgery/wound healing, and/or endocrine/growth disorders.

Finally, NOV9 is homologous to the thyroid regulated gene family of proteins. Thus, NOV9 nucleic acids and polypeptides, antibodies and related compounds according to the invention will be useful in therapeutic and diagnostic applications in various disorders including, for example, hypo- and hyperthyroidism, disorders of the thyroid, and thyroid-related cancers.

The NOVX nucleic acids and polypeptides can also be used to screen for molecules, which inhibit or enhance NOVX activity or function. Specifically, the nucleic acids and polypeptides according to the invention may be used as targets for the identification of small molecules that modulate or inhibit, *e.g.*, neurogenesis, cell differentiation, cell proliferation, hematopoiesis, wound healing and angiogenesis.

Additional utilities for the NOVX nucleic acids and polypeptides according to the invention are disclosed herein.

NOV1

A NOV1 sequence (also referred to as 30235661_EXT1) according to the invention includes a nucleic acid sequence encoding a polypeptide related to the testis specific serine/threonine protein kinase (TSK-1) family of proteins. Tables 1A and 1B show a NOV1 nucleic acid and its encoded polypeptide sequence, respectively. A disclosed NOV1 nucleic acid of 1149 nucleotides is shown in Table 1A. The disclosed NOV1 open reading frame (“ORF”) was identified beginning with an ATG initiation codon at nucleotides 1-3 and ending with a TAA codon at nucleotides 1147-1149. As shown in Table 1A, the start and stop codons are in bold letters.

Table 1A. NOV1 nucleotide sequence (SEQ ID NO:1).

ATGTCGGGAGACAACTTCTGAGCGAACTCGGTTATAAGCTGGGCCGCACAATTGGAGAGGGCAGCTACTCC
AAGGTGAAGGTGGCCACATCCAAGAAGTACAAGGGTACCGTGGCCATCAAGGTGGTGGACCGGCGGCGAGCG
CCCCGGAGTTTCGTCAACAAGTTCCTGCCGCGAGAGCTGTCCATCCTGCGGGGCGTGCGACACCGGCACATC
GTGCACGTCTTCGAGTTCATCGAGGTGTGCAACGGGAACTGTACATCGTGATGGAAGCGGCCGCCACCGAC
CTGCTGCAAGCCGTGCAGCGCAACGGGCGCATCCCCGGAGTTCAGGCGCGCGACCTCTTGCGCAGATCGCC
GGCGCCGTGCGCTACCTGCACGATCATCACCTGGTGCACCGCGACCTCAAGTGCGAAAACGTGCTGCTGAGC
CCGGACGAGCGCCGCGTCAAGCTCACCAGCTTCGGCTTCGGCCGCCAGGCCCATGGCTACCCAGACCTGAGC
ACCACCTACTGCGGCTCAGCCGCTACGCGTCACCCGAGGTGCTCCTGGGCATCCCCACGACCCCAAGAAG
TACGATGTGTGGAGCATGGGCGTCGTGCTCTACGTCATGGTCACCGGGTGCATGCCCTTCGACGACTCGGAC
ATCGCCGGCCTGCCCCGCGCCAGAAACGCGGCGTGCTCTATCCCGAAGGCCTCGAGCTGTCCGAGCGCTGC
AAGGCCCTGATCGCCGAGCTGCTGTCAGTTCAGCCCGTCCGCCAGGCCCTCCGCGGGCCAGGTAGCGCGCAAC
TGCTGGCTGCGCGCGGGGACTCCGGCAGGAACGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGA
GGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGA
AGAAAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGA
ATCCTTCAGAGTCTAAACTTCCTCGTGATACAACGTATAGCCACCCATTCCAGCCTGCTTATTGGAACCTC
TATCCCATCTGGTGGCAAACATTTCTTTTACATTTGTTTTACTATCAAAGATTTAGAGTCACAATAA

In a search of public sequence databases, it was found, for example, that the NOV1
 nucleic acid sequence disclosed in this invention has 219 of 314 bases (69 %) identical to one
 region of a *Homo Sapiens* DGS-G mRNA, 3' end, 1806 bp, with an E-value of $4.7e^{-37}$
 (GENBANK-ID: HUMDGS|acc:L77564). It also had 326 of 527 bp (61%) identical to a
 second region in this same sequence. Public nucleotide databases include all GenBank
 databases and the GeneSeq patent database.

In all BLAST alignments herein, the "E-value" or "Expect" value is a numeric
 indication of the probability that the aligned sequences could have achieved their similarity to
 the BLAST query sequence by chance alone, within the database that was searched. For
 example, the probability that the subject ("Sbjct") retrieved from the NOV1 BLAST analysis,
e.g., *Homo sapiens* DGS-G mRNA, matched the Query NOV1 sequence purely by chance is
 4.7×10^{-37} . The Expect value (E) is a parameter that describes the number of hits one can
 "expect" to see just by chance when searching a database of a particular size. It decreases
 exponentially with the Score (S) that is assigned to a match between two sequences.
 Essentially, the E value describes the random background noise that exists for matches between
 sequences.

The Expect value is used as a convenient way to create a significance threshold for
 reporting results. The default value used for blasting is typically set to 0.0001. In BLAST 2.0,
 the Expect value is also used instead of the P value (probability) to report the significance of
 matches. For example, an E value of one assigned to a hit can be interpreted as meaning that in
 a database of the current size one might expect to see one match with a similar score simply by
 chance. An E value of zero means that one would not expect to see any matches with a similar

score simply by chance. See, e.g., <http://www.ncbi.nlm.nih.gov/Education/BLASTinfo/>.

Occasionally, a string of X's or N's will result from a BLAST search. This is a result of automatic filtering of the query for low-complexity sequence that is performed to prevent artifactual hits. The filter substitutes any low-complexity sequence that it finds with the letter "N" in nucleotide sequence (e.g., "NNNNNNNNNNNNNN") or the letter "X" in protein sequences (e.g., "XXXXXXXXXX"). Low-complexity regions can result in high scores that reflect compositional bias rather than significant position-by-position alignment. Wootton and Federhen, *Methods Enzymol* 266:554-571, 1996.

A disclosed encoded NOV1 protein has 382 amino acid residues, referred to as the NOV1 protein. The NOV1 protein was analyzed for signal peptide prediction and cellular localization. The SignalP and Psort results predict that NOV1 does not have a signal peptide and is likely to be localized to the nucleus, with a certainty of 0.9800. The disclosed NOV1 polypeptide sequence is presented in Table 1B using the one-letter amino acid code.

Table 1B. Encoded NOV1 protein sequence (SEQ ID NO:2).

MSGDKLLSELGYKLGRTIGEGSYSKVKVATSKKYKGTVAIKVVDRRRAPPDFVNKFLPRELSILRGVRHPHI VHVFEFIEVCNGKLYIVMEAAATDLLQAVQRNGRIPGVQARDLFAQIAGAVRYLHDHHLVHRDLKCENVLLS PDERRVKLTDFGFRQAHGYPDLSSTTYCGSAAYASPEVLLGIPYDPKKYDVWSMGVVLYVMVTGCMFPDDSD IAGLPRRQKRGVLYPEGLELSERCKALIAELLQFSPSARPSAGQVARNCWLRAGDSGRNGRKRKEGREGRE GREGREGKEGKEGKGRKKREREGRKGKGRDKRKVQLTHHPFIILQSLKLPRDTTYSHPFPAYWNF YSHLVANISFYICFTIKDLESQ
--

NOV1 sequences were initially identified by searching a proprietary sequence file database for DNA sequences which translate into proteins with similarity to a protein family of interest. NOV1 was identified as having suitable similarity. NOV1 was analyzed further to identify any open reading frames encoding novel full length proteins, as well as, novel splice forms of TSK-1. This was done by extending the identified NOV1 using suitable sequences from additional proprietary assemblies, publicly available EST sequences and public genomic sequences. A Genomic clone AC011448 was identified as having regions with 100% identity to the NOV1 and was selected for analysis because this identity implied that this clone contained the sequence of the genomic locus for NOV1.

The genomic clones were analysed by Genscan and Grail to identify exons and putative coding sequences/open reading frames. This clone was also analyzed by TblastN, BlastX and other homology programs to identify regions translating to proteins with similarity to the

original protein/protein family of interest. Expressed sequences from both public and proprietary databases were also added when available to further define and complete the gene sequence. The DNA sequence was then manually corrected for apparent inconsistencies thereby obtaining the sequences encoding the full-length protein.

5 The TSK-1 disclosed in this invention (NOV1) belongs to genomic DNA [AC011448 from GenbankNEW]. Within this GenbankNew entry was a note showing that the sequence was from Chromosome 19. Therefore we assign the chromosomal locus of NOV1 as Chromosome 19. Further, the TSK-1 disclosed in this invention (NOV1) is expressed in testis.

10 A BLASTX search was performed against public protein databases. The disclosed NOV1 protein (SEQ ID NO:2) has good identity with TSK-1-like proteins. For example, the full amino acid sequence of the protein of the invention was found to have 146 of 360 amino acid residues (40 %) identical to, and 208 of 360 residues (57 %) similar to, the 364 amino acid residue TSK-1 protein from *Mus musculus* (SPTREMBL-ACC:Q61241; E= 3.4 e-66). Public amino acid databases include the GenBank databases, SwissProt, PDB and PIR.

15 It was also found that NOV1 had homology to the amino acid sequences shown in the BLASTP data listed in Table 1C.

Table 1C. BLAST results for NOV1					
Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
gi 14042966 ref NP_114426.1	serine/threonine protein kinase SSTK [Homo sapiens]	273	272/272 (100%)	272/272 (100%)	1e-152
gi 13540326 gb AAK29414.1 AF348077_1 (AF348077)	serine/threonine kinase FKSG82 [Homo sapiens]	273	272/272 (100%)	272/272 (100%)	1e-152
gi 13898617 gb AAK48827.1 AF329483_1 (AF329483)	serine/threonine protein kinase SSTK [Homo sapiens]	273	272/272 (100%)	272/272 (100%)	1e-152
gi 14030781 ref NP_114393.1	serine/threonine protein kinase SSTK [Mus musculus]	273	264/272 (97%)	270/272 (99%)	1e-148
gi 13898619 gb AAK48828.1 AF329484_1 (AF329484)	serine/threonine protein kinase SSTK [Mus musculus]	273	264/272 (97%)	270/272 (99%)	1e-148

The homology of these and other sequences is shown graphically in the ClustalW analysis shown in Table 1D. In the ClustalW alignment of the NOV1 protein, as well as all other ClustalW analyses herein, the black outlined amino acid residues indicate regions of conserved sequence (*i.e.*, regions that may be required to preserve structural or functional properties), whereas non-highlighted amino acid residues are less conserved and can potentially be mutated to a much broader extent without altering protein structure or function.

Table 1D. ClustalW Analysis of NOV1

1) Novel NOV1 (SEQ ID NO:2)	
2) gi 14042966 ref NP_114426.1 serine/threonine protein kinase SSTK [Homo sapiens] (SEQ ID NO:35)	
3) gi 14030781 ref NP_114393.1 serine/threonine protein kinase SSTK [Mus musculus] (SEQ ID NO:36)	
4) gi 12860201 dbj BAB31876.1 putative [Mus musculus] (SEQ ID NO:37)	
5) gi 14042947 ref NP_114417.1 serine/threonine kinase FKSG81 [Homo sapiens] (SEQ ID NO:38)	
6) gi 6678165 ref NP_033461.1 testis-specific serine/threonine kinase [Mus musculus] (SEQ ID NO:31)	

102030405060

NOV1

gi|14042966|

gi|14030781|

gi|12860201|

gi|14042947|

gi|6678165|

MSGDKLLSELGYKLGRTIGEGSYSKVKVATSKKKYKGTVAIKVVDRRRAPDFVNKFLPRE
MSGDKLLSELGYKLGRTIGEGSYSKVKVATSKKKYKGTVAIKVVDRRRAPDFVNKFLPRE
MSGDKLLSELGYKLGRTIGEGSYSKVKVATSKKKYKGTVAIKVVDRRRAPDFVNKFLPRE
--MEDFLLSNGYLGKTTIGGTYSKVKEAFSKKHQRKVAIKIIDKMGGPEEFQRFLLPRE
MDDAAVLKRRGYLLGINLGEYSYAKVKSAYSERLKFNVVAIKIIDKKAPSDFLEKFLPRE
MDDAAVLKRRGYLLGINLGEYSYAKVKSAYSERLKFNVVAIKIIDKKAPSDFLEKFLPRE

708090100110120

NOV1

gi|14042966|

gi|14030781|

gi|12860201|

gi|14042947|

gi|6678165|

LSILRGVRHPHIVHVFEEFIEVCNGKLYIVMEAAAT--DLLQAVQRNGRIPGVQARDLFAQI
LSILRGVRHPHIVHVFEEFIEVCNGKLYIVMEAAAT--DLLQAVQRNGRIPGVQARDLFAQI
LSILRGVRHPHIVHVFEEFIEVCNGKLYIVMEAAAT--DLLQAVQRNGRIPGVQARDLFAQI
LQIVRTLDHKNITQVYEMLESADGKIYIVMELAEAGGDVFDCLVNGGFLPESRAKALEROM
TEILAMLNHSIILKTYEIEFTSHGKQYIVMELAVCGDLEELIKTRGALHEDEPARKKHOL
TEILAMLNHSIIVKTYEIEFTSHGKQYIVMELAVCGDLEELIKTRGALHEDEPARKKHOL

130140150160170180

NOV1

gi|14042966|

gi|14030781|

gi|12860201|

gi|14042947|

gi|6678165|

AGAVRYLHDHHLVHRDLKCENVLLSPDERRVKLTDFGFGROAHG----YPDLSSTTYCGSA
AGAVRYLHDHHLVHRDLKCENVLLSPDERRVKLTDFGFGROAHG----YPDLSSTTYCGSA
AGAVRYLHDHHLVHRDLKCENVLLSPDERRVKLTDFGFGROAHG----YPDLSSTTYCGSA
VEATRYCHGCCVAHRDLKCENALLQG--FNILKLTDFGFGKVLPKS---RRRLSOTFCGST
SLATRYCHDLDVVHRDLKCNELLDKD--FNILKLSDFSFSLRCLRDDSGRMALSKTFCGSP
SLATRYCHDLDVVHRDLKSENELLDKD--FNILKLSDFGFSRCLRDDSGPLILSKTFCGSA

190200210220230240

NOV1

gi|14042966|

gi|14030781|

gi|12860201|

gi|14042947|

gi|6678165|

AYASPEVLLGIPYDPKKYDVWSMGVVLYVMVTGCMFPDDSDIAG--LPRRQKRGVLYPEGL
AYASPEVLLGIPYDPKKYDVWSMGVVLYVMVTGCMFPDDSDIAG--LPRRQKRGVLYPEGL
AYASPEVLLGIPYDPKKYDVWSMGVVLYVMVTGCMFPDDSDIAG--LPRRQKRGVLYPEGL
AYAAPEVLQGIPIHDSKKGDVWSMGVVLYVMVLCASLPFDQDIPK--MLWQQQKGVSFPTHL
AYAAPEVLQGIPIYQPKVYDIWSLGVILYIMVCGSMPIYDDSNIKKMLRIQKEHRVNFPRSK
AYAAPEVLQGIPIYQPKVYDIWSLGVILYIMVCGSMPIYDDSNIKK--LRIQKEHRVNFPRSK

250260270280290300

NOV1

gi|14042966|

gi|14030781|

gi|12860201|

gi|14042947|

gi|6678165|

ELSERCKALIAELLQFSPSARPSAGQVARNCWLRAGDSC--RNGRKGRKEGREGREGREGRE
ELSERCKALIAELLQFSPSARPSAGQVARNCWLRAGDSC--RNGRKGRKEGREGREGREGRE
ELSERCKSLIAELLQFSPSARPSAGQVARNCWLRAGDSC-----
GISTECQDLKRLLEPDMILRPSIEEVSWHPELWAST-----
HLTGCKDLIYHMLQPDVNRRLHIDEILLSHCWMPKARGSPSVAINKEGESSFGTEPLWT
HLTGCKDLIYHMLQPDVNRRLHIDEILLNHCWMPKARGSLSSGAINKEGESSFATEPSWI

310320330340350360

5

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15

20

30

gnl|Smart|S TKc, Serine/Threonine protein kinases, catalytic domain (Phosphotransferases. Serine or threonine-specific kinase subfamily) (SEQ ID NO:40)
CD-Length = 256 residues, 100.0% aligned
Score = 231 bits (590), Expect = 4e-62 .

35

40

		70	80	90	100	110	120
5	NOV1	PRELSILRGVRRHPIVHVFEFIEVCN-----GKLYIVME-AAATDLQAVQRNGRIPGV					
	SMART_STKc Domain	-REIKILKKLDHPNIVKLYDVFEF-D-----DKLYIVMEYCEGGDLFDLLKKRGRLED					
		130	140	150	160	170	180
10	NOV1	QARDLFAQTAGAVRYLHDH-HLVHRDLKCENVLLSPDE--RRVKLTDFGFGRCAGGYP-D					
	SMART_STKc Domain	EARFYARQILSALEYLHSQ-GIIHRDLKPENILLDSQ---GHVKLADFGGLAKQLDSSG-T					
		190	200	210	220	230	240
15	NOV1	LSTTYCGSAAAYASPEVLL-GIPYDPR-KYDVWSMGVLYVMVTCMPFDDSDS-----DIAG					
	SMART_STKc Domain	LLTTEVGTPEYMAPEVLL-GKGYG-R-AVDHWSLGVILYELITGRPPFPGD-----DQLL					
		250	260	270	280	290	300
20	NOV1	LPRRQKRGVLY---EEGLE-----LSE					
	SMART_STKc Domain	ALFKKIGKPKPPFPPEWK-----ISP					
		310	320	330			
25	NOV1	RCRA-LTAEILLQFSFSARPSAGQVAR-----NCWL					
	SMART_STKc Domain	EAKD-LIKKILLVKDPEKRLTAEEALK-----HPEF					

Table 1F. Domain Analysis of NOV1

gnl|Pfam|pfam00069, pkinase, Protein kinase domain.(SEQ ID NO:41)
 CD-Length = 256 residues, 100.0% aligned
 Score = 201 bits (511), Expect = 6e-53

		10	20	30	40	50	60
30	NOV1	YKLGRTIGEGSYSKVKVATSKK--YKGTVAIKVVD-----ERRAPPDFV--NKFL					
	Pfam_pfam00069	YELGEKLGSGAFCKVYKGKHKD--TGEIVAIKILK-----KESLSEKKK--R--F					
		70	80	90	100	110	120
35	NOV1	PRELSILRGVR-----HPHIVHVFEFIE--VCNGKLYIVME-AAAT--DLQAVQRNG					
	Pfam_pfam00069	LREIQILRRIS-----HENIVRRLGVFE--E-DDHLYIVMEYMEGG--DLFDYLRRNG					
		130	140	150	160	170	180
40	NOV1	-RTPGVQARDLFAQTAGAVRYLHDHHLVHRDLKCENVLLSPDE--RRVKLTDFGFGRC					
	Pfam_pfam00069	LLLSEKEAKKTALQILRGLEYLHSRGIVHRDLKPENILLD-EN---GTVKLTADFGGLARK					
		190	200	210	220	230	240
45	NOV1	AHGYPD-LSTTYCGSAAAYASPEV-----LLG-----IPYDPRKYDVWSMGVLYVMV					
	Pfam_pfam00069	LESSSYEKLTTTEVGTPEYMAPEV-----LEG-----RGYSS-KVDVWSLGVILYEL					
		250	260	270	280	290	300
50	NOV1	TG-----CMPFDD-----SDIAG--LPRRQKR-----GVLY					
	Pfam_pfam00069	TG-----KLPPFG-----IDPLEELFRIKERP-----RIIR					
		310	320	330			
55	NOV1	YEGLLELSERCALIAELLQFSFSARPSAGQVARNCWL					
	Pfam_pfam00069	LPLPPNCSEELKDLIKKCLNKDPEKRLTAKEILLNHPWF					

Table 1G. Domain Analysis of NOV1

gnl|Smart|TyrKc, Tyrosine kinase, catalytic domain
 (Phosphotransferases. Tyrosine-specific kinase subfamily) (SEQ
 ID NO:42)
 CD-Length = 257 residues, 98.1% aligned
 Score = 126 bits (316), Expect = 2e-30

5	NOV110.....20.....30.....40.....50.....60
	SMART_TyrKc	YKLGRTTIGEGSYSKVKVATSKKYKG---T---VATKVVDRRRAPPD---FVNKFLPREL
10	NOV170.....80.....90.....100.....110.....120
	SMART_TyrKc	SLTRGV-RHPHIVHVFEFIEVC--N--GKLYIVME-AAATDLLQAVORNGRIPG-----
15	NOV1130.....140.....150.....160.....170.....180
	SMART_TyrKc	-----MQARDLFA--QIAGAVRYLHDH--HLVHRDLKENVLESPDE
20	NOV1190.....200.....210.....220.....230.....240
	SMART_TyrKc	R-----RVKLTDFGFGROAHGY-PDLSTT-YCG-SA-AYASPEVLLGIPYDPKDYDV
25	NOV1250.....260.....270.....280.....290.....300
	SMART_TyrKc	WSMGVVLIVVMVTGC-MPEHDD-----SDIAGLPRROKRGVLYPEGLELSERC
30	NOV1310.....320.....330
	SMART_TyrKc	KALTAELT---QFSPSARPSAGOVARNCW
	SMART_TyrKc	PDELYDLMLQCWAEDPEDRPTFSEL-VERL

BLAST results include sequences from the Patp database, which is a proprietary
 database that contains sequences published in patents and patent publications. Patp results
 include those listed in Table 1H.

Table 1H. Patp alignments of NOV1

Sequences producing High-scoring Segment Pairs:	Smallest Sum		
	Reading Frame	High Score	Prob. P(N)
Patp:AAB65686 Novel Protein Kinase <i>Homo Sapiens</i> , 273 aa	+1	1429	1.8e-145
Patp:AAB42167 Human ORFX ORF1931 polypeptide, 210 aa	+1	910	1.8e-90

For example, a BLAST against patp: AAB65686 (WO00/073469), a 273 amino acid
 protein kinase from *Homo sapiens*, produced good identity, E = 1.8e-145. Additionally, a

BLAST against patp: AAB42167, a 210 Human ORFX polypeptide sequence (WO00/058473), also produced good identity, $E=1.8E-90$.

Protein kinases are involved in intracellular signal transduction pathways. They are broadly classified into serine/threonine kinases and tyrosine kinases, which can be further divided into families and subfamilies based on similarity within the catalytic domain.

Two studies have isolated and identified members of the testis specific serine/threonine protein kinase family. Bielke et al. (1994) isolated a cDNA fragment encoding a new member of the Ser/Thr (serine/threonine) family of protein kinases using degenerate oligos corresponding to two highly conserved motifs within the protein kinase catalytic domain and a PCR-based cloning strategy. Expression analysis revealed that the fragment recognized two transcripts (1.6 and 1.4 kb) exclusively in testis. Using this fragment as a probe, Bielke et al. (1994) cloned a full-length cDNA from a mouse testis cDNA library. The sequence has a 1092-bp open reading frame encoding a protein of 364 amino acids. The N-terminally localized kinase catalytic domain has all the conserved motifs found in other Ser/Thr kinases. Northern blot analysis using the full-length sequence as a probe revealed that the cloned gene corresponds to the 1.6-kb transcript, suggesting the existence of at least two testis-specific novel Ser/Thr kinases. Bielke et al. (1994) proposed the name testis-specific kinase-1 (TSK-1) for the identified/described gene. A GenEMBL databank search revealed highest homology to the human gene encoding rac protein kinase-beta and the group of yeast Ser/Thr kinases encoded by SNF-1, nim-1, KIN-1 and KIN-2.

In a more recent study, Rosok et al. (1999) isolated a novel full-length cDNA from a human fetal liver cDNA library using a subtractive PCR cloning strategy and degenerate primers based on conserved amino acid regions in the catalytic domain of serine/threonine kinases. Rosok et al. (1999) designated the cDNA testis-specific kinase-2 (TESK2) because it encodes a putative 555-amino acid protein with a kinase domain that is 65% identical to that of testis-specific kinase-1 (TESK1), which exhibits dual specific protein kinase activity on both serine/threonine and tyrosine; it also shows 42% and 39% identity to LIMK1 and LIMK2, respectively. Northern blot analysis revealed a single TESK2 mRNA species of approximately 3.0 kb, predominantly expressed in testis and prostate. Rosok et al. (1999) also found that the rat homolog was first expressed in the testis after day 30 of postnatal development in round spermatids. The authors suggested that TESK2 plays an important role in spermatogenesis.

The above defined information for this invention suggests that this novel TSK-1-like protein (NOV1) may function as a member of a TSK-1 family. Therefore, the expression nucleic acids and proteins of NOV1 are useful in potential therapeutic applications implicated in various TSK-1-related pathologies and/or disorders. For example, a cDNA encoding the TSK-1-like protein may be useful in gene therapy, and the TSK-1-like protein may be useful when administered to a subject in need thereof. The novel nucleic acid encoding NOV1 protein, or fragments thereof, may further be useful in diagnostic applications, wherein the presence or amount of the nucleic acid or the protein are to be assessed. These materials are further useful in the generation of antibodies that bind immunospecifically to the novel substances of the invention for use in therapeutic or diagnostic methods.

The NOVX nucleic acids and proteins of the invention are useful in potential therapeutic applications implicated in various diseases and disorders described below and/or other pathologies and disorders. For example, but not limited to, a cDNA encoding the TSK-1-like protein may be useful in gene therapy, and the TSK-1-like protein may be useful when administered to a subject in need thereof. By way of nonlimiting example, the compositions of the present invention will have efficacy for treatment of patients suffering from Spermatogenesis, Male Reproductive Health, Fertility and/or other pathologies/disorders. The novel nucleic acid encoding the TSK-1-like protein, and the TSK-1-like protein of the invention, or fragments thereof, may further be useful in diagnostic applications, wherein the presence or amount of the nucleic acid or the protein are to be assessed. These materials are further useful in the generation of antibodies that bind immunospecifically to the novel substances of the invention for use in therapeutic or diagnostic methods.

Further, the protein similarity information, expression pattern, and map location for NOV1 suggests that NOV1 may have important structural and/or physiological functions characteristic of the TSK-1 family. Therefore, the nucleic acids and proteins of the invention are useful in potential diagnostic and therapeutic applications and as a research tool. Potential therapeutic uses for the compositions of the invention included, for example but not limited to, the following: (i) Protein therapeutic, (ii) small molecule drug target, (iii) antibody target (therapeutic, diagnostic, drug targeting/cytotoxic antibody), (iv) diagnostic and/or prognostic marker, (v) gene therapy (gene delivery/gene ablation), (vi) research tools, and (vii) tissue regeneration *in vitro* and *in vivo* (regeneration for all these tissues and cell types composing these tissues and cell types derived from these tissues).

These materials are further useful in the generation of antibodies that bind immuno-specifically to the novel NOV1 substances for use in therapeutic or diagnostic methods. These antibodies may be generated according to methods known in the art, using prediction from hydrophobicity charts, as described in the "Anti-NOVX Antibodies" section below. The disclosed NOV1 protein has multiple hydrophilic regions, each of which can be used as an immunogen. In one embodiment, a contemplated NOV1 epitope is from about amino acids 10 to 30. In another embodiment, a NOV1 epitope is from about amino acids 35 to 70. In additional embodiments, NOV1 epitopes are from amino acids 90 to 110, 120-170, 180-190, 210-230, 250-335 and from amino acids 340 to 365. These novel proteins can be used in assay systems for functional analysis of various human disorders, which will help in understanding of pathology of the disease and development of new drug targets for various disorders.

NOV2

NOV2 includes three novel beta thymosin-like proteins disclosed below. The disclosed proteins have been named NOV2a, NOV2b and NOV2c.

NOV2a

A novel nucleic acid was identified on chromosome 9 by TblastN using CuraGen Corporation's sequence file for beta thymosin or homolog as run against the Genomic Daily Files made available by GenBank or from files downloaded from the individual sequencing centers. The nucleic acid sequence was predicted from the genomic file GB ACCNO:ba518k17 by homology to a known beta thymosin or homolog. Exons were predicted by homology and the intron/exon boundaries were determined using standard genetic rules. Exons were further selected and refined by means of similarity determination using multiple BLAST (for example, tBlastN, BlastX, and BlastN) searches, and, in some instances, GeneScan and Grail. Expressed sequences from both public and proprietary databases were also added, when available, to further define and complete the gene sequence. The DNA sequence was then manually corrected for apparent inconsistencies thereby obtaining the sequences encoding the full-length protein. In particular, nucleotide 121905 was spliced to nucleotide 121758 in preparing the ba518k17_A sequence.

The novel nucleic acid of 147 nucleotides (also referred to as ba518k17_A) encoding a novel beta thymosin-like protein is shown in Table 2A. An open reading frame was identified beginning with an ATG initiation codon at nucleotides 6-8 and ending with a TGA codon at

nucleotides 135-137. A putative untranslated region upstream from the initiation codon and downstream from the termination codon is underlined in Table 2A, and the start and stop codons are in bold letters.

Table 2A. NOV2a Nucleotide Sequence (SEQ ID NO:3)

<p><u>AGAAAATGGCACACAACTAGACCTGGAAGAAATTGCCAGCTTGGATAAGGCCAAGCTGAAGGCCACAGAG</u> <u>ATGCAGAAGAACA</u>CTCTGATGACCAAAGAGACCACAGAGCAGGAGAAGTGGAGTGAAATTCCTTGAGAGCC <u>TCGAG</u></p>

In a search of public sequence databases, it was found, for example, that the nucleic acid sequence (NOV2a) has 126 of 150 bases (84%) identical to a human beta thymosin mRNA (GENBANK-ID: S54005|acc:S54005) (E = 7.0 e-17). Public nucleotide databases include all GenBank databases and the GeneSeq patent database.

The disclosed NOV2a polypeptide (SEQ ID NO:4) encoded by SEQ ID NO:3 is 43 amino acid residues and is presented using the one-letter code in Table 2B. The NOV2a protein was analyzed for signal peptide prediction and cellular localization. SignalP, Psort and Hydropathy results predict that NOV2a does not appear to contain a predicted signal peptide and that NOV2a is likely to be localized in the cytoplasm with a certainty of 0.4500.

Table 2B. Encoded NOV2a protein sequence (SEQ ID NO:4).

<p>MAHKLDLEEIASLDKAKLKATEMQNTLMTKETTEQEKWSEIS</p>

The full amino acid sequence of the NOV2a protein of the invention was found to have 33 of 44 amino acid residues (75%) identical to, and 34 of 44 residues (77%) positive with, the 44 amino acid residue Thymosin beta-10 protein from rat (ptnr: PIR-ID:A27266; E = 7.2 e-09)(Table 2C). The global sequence homology is 79% amino acid similarity and 77% amino acid identity. In addition, this protein contains the thymosin protein domain (as defined by Interpro# IPR001152) at amino acid positions 2 to 41. Public amino acid databases include the GenBank databases, SwissProt, PDB and PIR.

Table 2C. BLASTX results for NOV2a

Sequences producing High-scoring Segment Pairs:	Reading Frame	High Score	Smallest Sum Prob	
			P (N)	N
ptnr:PIR-ID:A27266 thymosin beta-10 - rat	+3	137	7.2e-09	1

NOV2b

In the present invention, the target sequence identified above, Accession Number ba518k17_A, was subjected to the exon linking process to confirm the sequence. PCR primers were designed by starting at the most upstream sequence available, for the forward primer, and at the most downstream sequence available for the reverse primer. In each case, the sequence was examined, walking inward from the respective termini toward the coding sequence, until a suitable sequence that is either unique or highly selective was encountered, or, in the case of the reverse primer, until the stop codon was reached. Such suitable sequences were then employed as the forward and reverse primers in a PCR amplification based on a wide range of cDNA libraries. The resulting amplicon was gel purified, cloned and sequenced to high redundancy to provide the sequence reported below, which is designated Accession Number 518k17_A1.

A disclosed NOV2b (also referred to as 518k17_A1) nucleic acid of 147 nucleotides is shown in Table 2D. An open reading frame was identified beginning with an ATG initiation codon at nucleotides 6-8 and ending with a TGA codon at nucleotides 135-137. A putative untranslated region upstream from the initiation codon and downstream from the termination codon is underlined in Table 2D, and the start and stop codons are in bold letters.

Table 2D. NOV2b Nucleotide Sequence (SEQ ID NO:5)

AGAAAA**TGG**CACACAACTAGACCTGGAAGAAATTGCCAGCTTGGATAAGGCCAAGCTGAAGGCCACAGAG
ATGCAGAAGAACTCTGATGACCAAGAGACCACAGAGCAGGAGAAGTGGAGTGAAATTTCT**TGAGAGCC**
TCGAG

The disclosed NOV2b polypeptide (SEQ ID NO:6) encoded by SEQ ID NO:5 is 43 amino acid residues and is presented using the one-letter code in Table 2E. The NOV2b protein was analyzed for signal peptide prediction and cellular localization. SignalP, Psort and Hydropathy results predict that NOV2b does not appear to contain a predicted signal peptide and that NOV2b is likely to be localized in the cytoplasm with a certainty of 0.4500. NOV2b has a molecular weight of 4979.7 Daltons.

Table 2E. Encoded NOV2b protein sequence (SEQ ID NO:6).

MAHKLDLEETIASLDAKALKATEMQKNTLMTKETTEQEKEWSEIS

The amino acid sequence of NOV2b had high homology to other proteins as shown in Table 2F.

5

Table 2F. BLASTX results for NOV2b

Sequences producing High-scoring Segment Pairs:	Reading Frame	High Score	Smallest Sum Prob P(N)	N
ptnr:PIR-ID:A27266 thymosin beta-10 - rat	+3	137	1.8e-08	1
ptnr:SWISSPROT-ACC:P13472 THYMOSIN BETA-10 - Homo sapi...	+3	132	6.0e-08	1
ptnr:TREMBLNEW-ACC:BAA96493 THYMOSIN BETA B - Cyprinus...	+3	115	3.8e-06	1
ptnr:SWISSPROT-ACC:P21752 THYMOSIN BETA-9 AND BETA-8 -...	+3	114	4.9e-06	1
ptnr:SPTREMBL-ACC:Q9PT32 THYMOSIN BETA - Oncorhynchus ...	+3	113	6.2e-06	1
ptnr:TREMBLNEW-ACC:CAB76965 PUTATIVE THYMOSIN BETA-10 ...	+3	113	6.2e-06	1
ptnr:SWISSPROT-ACC:P21753 THYMOSIN BETA-9 - Sus scrofa...	+3	112	7.9e-06	1
ptnr:SWISSPROT-ACC:P26351 THYMOSIN BETA-11 - Oncorhync...	+3	108	2.1e-05	1
ptnr:PIR-ID:S21282 thymosin beta-11 - rainbow trout	+3	108	2.1e-05	1
ptnr:SPTREMBL-ACC:O76538 THYMOSIN BETA - Strongylocent...	+3	107	2.7e-05	1
ptnr:PIR-ID:A59005 thymosin beta - sea urchin (Arbacia...	+3	106	3.4e-05	1
ptnr:PIR-ID:JQ1489 thymosin beta-4 - African clawed frog	+3	104	5.6e-05	1
ptnr:PIR-ID:B59005 thymosin beta - scallop (Argopecten...	+3	103	7.1e-05	1
ptnr:SPTREMBL-ACC:Q9W7M8 BETA-THYMOSIN - Brachydanio r...	+3	102	9.1e-05	1
ptnr:SWISSPROT-ACC:P26352 THYMOSIN BETA-12 - Oncorhync...	+3	101	0.00012	1
ptnr:PIR-ID:S22426 thymosin beta-12 - rainbow trout	+3	101	0.00012	1
ptnr:TREMBLNEW-ACC:CAB94229 DJ1071L10.1 (THYMOSIN/INTE...	+3	100	0.00015	1
ptnr:SWISSPROT-ACC:P20065 THYMOSIN BETA-4 - Mus muscul...	+3	99	0.00019	1

Possible SNPs found for NOV2b are listed in Table 2G.

Table 2G: SNPs

Base Position	Base Before	Base After
238	A	C(2)
241	C	A(2)
251	A	C(3)
253	A	G(3)
254	C	G(3)
255	C	T(3)
266	C	T(2)
572	C	T(2)
673	G	T(3)
748	C	T(2)

NOV2c

In the present invention, the target sequence identified above, Accession Number ba518k17_A, was subjected to the exon linking process to confirm the sequence. PCR primers were designed by starting at the most upstream sequence available, for the forward primer, and at the most downstream sequence available for the reverse primer. In each case, the sequence was examined, walking inward from the respective termini toward the coding sequence, until a suitable sequence that is either unique or highly selective was encountered, or, in the case of the reverse primer, until the stop codon was reached. Such suitable sequences were then employed as the forward and reverse primers in a PCR amplification based on a wide range of cDNA libraries. The resulting amplicon was gel purified, cloned and sequenced to high redundancy to provide the sequence reported below, which is designated Accession Number 518k17_A.

A disclosed NOV2c (also referred to as 518k17_A) nucleic acid of 147 nucleotides is shown in Table 2H. An open reading frame was identified beginning with an ATG initiation codon at nucleotides 6-8 and ending with a TGA codon at nucleotides 135-137. A putative untranslated region upstream from the initiation codon and downstream from the termination codon is underlined in Table 2H, and the start and stop codons are in bold letters.

Table 2H. NOV2c Nucleotide Sequence (SEQ ID NO:7)

AGAAA AT GGCACACAACTAGACCTGGAAGAAATTGCCAGCTTGGATAAGGCCAAGCTGAAGGCCACAGAG ATGCAGAAGAACA CT CTGATGACCAAGAGACCACAGAGCAGGAGAAGTGGAGTGAAATTT CTGAGAGCC TCGAG

The disclosed NOV2c polypeptide (SEQ ID NO:8) encoded by SEQ ID NO:7 is 43 amino acid residues and is presented using the one-letter code in Table 2I. The NOV2c protein was analyzed for signal peptide prediction and cellular localization. SignalP, Psort and Hydropathy results predict that NOV2c does not appear to contain a predicted signal peptide and that NOV2c is likely to be localized in the cytoplasm with a certainty of 0.4500. NOV2c has a molecular weight of 4979.7 Daltons.

Table 2I. Encoded NOV2c protein sequence (SEQ ID NO:8).

MAHKLDLEEIASLDKAKLKATEMQKNTLMTKETTEQEKWSEIS

The amino acid sequences of NOV2c had high homology to other proteins as shown in Table 2J.

Table 2J. BLASTX results for NOV2c					
Sequences producing High-scoring Segment Pairs:	Reading Frame	High Score	Smallest Sum Prob P(N)	N	
ptnr:PIR-ID:A27266 thymosin beta-10 - rat	+3	137	1.7e-08	1	
ptnr:SWISSPROT-ACC:P13472 THYMOSIN BETA-10 - Homo sapi...	+3	132	5.9e-08	1	
ptnr:TREMBLNEW-ACC:BAA96493 THYMOSIN BETA B - Cyprinus...	+3	115	3.7e-06	1	
ptnr:SWISSPROT-ACC:P21752 THYMOSIN BETA-9 AND BETA-8 -...	+3	114	4.8e-06	1	
ptnr:SPTREMBL-ACC:Q9PT32 THYMOSIN BETA - Oncorhynchus ...	+3	113	6.1e-06	1	
ptnr:TREMBLNEW-ACC:CAB76965 PUTATIVE THYMOSIN BETA-10 ...	+3	113	6.1e-06	1	
ptnr:SWISSPROT-ACC:P21753 THYMOSIN BETA-9 - Sus scrofa...	+3	112	7.8e-06	1	
ptnr:SWISSPROT-ACC:P26351 THYMOSIN BETA-11 - Oncorhync...	+3	108	2.1e-05	1	
ptnr:PIR-ID:S21282 thymosin beta-11 - rainbow trout	+3	108	2.1e-05	1	
ptnr:SPTREMBL-ACC:O76538 THYMOSIN BETA - Strongylocent...	+3	107	2.6e-05	1	
ptnr:PIR-ID:A59005 thymosin beta - sea urchin (Arbacia...	+3	106	3.4e-05	1	
ptnr:PIR-ID:JQ1489 thymosin beta-4 - African clawed frog	+3	104	5.5e-05	1	
ptnr:PIR-ID:B59005 thymosin beta - scallop (Argopecten...	+3	103	7.0e-05	1	
ptnr:SPTREMBL-ACC:Q9W7M8 BETA-THYMOSIN - Brachydanio r...	+3	102	8.9e-05	1	
ptnr:SWISSPROT-ACC:P26352 THYMOSIN BETA-12 - Oncorhync...	+3	101	0.00011	1	
ptnr:PIR-ID:S22426 thymosin beta-12 - rainbow trout	+3	101	0.00011	1	
ptnr:TREMBLNEW-ACC:CAB94229 DJ1071L10.1 (THYMOSIN/INTE...	+3	100	0.00015	1	
ptnr:SWISSPROT-ACC:P20065 THYMOSIN BETA-4 - Mus muscul...	+3	99	0.00019	1	
ptnr:TREMBLNEW-ACC:AAC52490 THYMOSIN B4 - Mus musculus...	+3	99	0.00019	1	

NOV2a, 2b and 2c are related to each other as shown in the alignment listed in Table 2K.

Table 2K: ClustalW of NOV2 Variants

		10	20	30	40	50	60
10	NOV2A	AGAAAATGGCACACAACTAGACCTGGAAGAAATTGCCAGCTTGGATAAGGCCAAGCTGA					
	NOV2B	AGAAAATGGCACACAACTAGACCTGGAAGAAATTGCCAGCTTGGATAAGGCCAAGCTGA					
	NOV2C	AGAAAATGGCACACAACTAGACCTGGAAGAAATTGCCAGCTTGGATAAGGCCAAGCTGA					
15		70	80	90	100	110	120
	NOV2A	AGGCCACAGAGATGCAGAAAGAACTCTGATGACCAAAGAGACCACAGAGCAGGAGAAGT					
	NOV2B	AGGCCACAGAGATGCAGA=GAACACTCTGATGACCAAAGAGACCACAGAGCAGGAGAAGT					
	NOV2C	AGGCCACAGAGATGCAGAAAGAACTCTGATGACCAAAGAGACCACAGAGCAGGAGAAGT					
20		130	140				
	NOV2A	GGAGTGAAATTTCTCTGAGAGCCTCGAG					
	NOV2B	GGAGTGAAATTTCTCTGAGAGCCTCGAG					
	NOV2C	GGAGTGAAATTTCTCTGAGAGCCTCGAG					
25							

It was also found that NOV2a had homology to the amino acid sequences shown in the BLASTP data listed in Table 2L.

Table 2L. BLAST results for NOV2a

Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
gi 339697 gb AAA367 46.1 (M92383)	thymosin beta-10 [Homo sapiens]	49	33/44 (75%)	34/44 (77%)	6.1

The homology of these sequences is shown graphically in the ClustalW analysis shown in Table 2M.

Table 2M. ClustalW Analysis of NOV2a

- 2) gi|339697|gb|AAA36746.1| thymosin beta-10 [Homo sapiens] (SEQ ID NO:43)

.....|.....|.....|.....|.....|.....|.....|.....|.....|.....
10 20 30 40
NOV2A -----MAHKLDEEEIASLDAKALKATEMC-KNTIMTKETIEQEKRWSEIS
gi|339697| DCFKKMADKPOMGEIASFDKAKLKKTETOEKNTLEPTKETIEQEKRWSEIS

Other BLAST results include sequences from the Patp database, which is a proprietary database that contains sequences published in patents and patent publications. Patp results include those listed in Table 2N.

Table 2N. Patp alignments of NOV2

Sequences producing High-scoring Segment Pairs:				Smallest Sum
		Reading Frame	High Score	Prob. P (N)
Patp:AAR96932	Thymosin beta 10- synthetic, 43 aa	+3	132	4.9e-8
Patp:AAY80267	Thymosin beta 4 peptide isoform, 43 aa	+3	132	4.9e-8

For example, a BLAST against patp:AAR96932, a 43 amino acid synthetic thymosin beta 10 protein (WO96/11016), produced good identity, $E=4.9e-8$. Additionally, a BLAST against patp:AAY80267, a thymosin beta 4 peptide isoform (Tbeta10) (WO00/06190), a 43 amino acid polypeptide, also produced good identity, $E=4.9e-8$.

Thymosin-beta-4 (T-beta-4) induces the expression of terminal deoxynucleotidyl transferase activity in vivo and in vitro, inhibits the migration of macrophages, and stimulates the secretion of hypothalamic luteinizing hormone-releasing hormone. Clauss et al. (1991) noted that the protein was originally isolated from a partially purified extract of calf thymus,

thymosin fraction 5, which induced differentiation of T cells and was partially effective in some immuno-compromised animals. Further studies demonstrated that the molecule is ubiquitous in all tissues and cell lines analyzed. It is found in highest concentrations in spleen, thymus, lung, and peritoneal macrophages. Li et al. (1996) stated that T-beta-4 is an actin monomer sequestering protein that may have a critical role in modulating the dynamics of actin polymerization and depolymerization in nonmuscle cells. Its regulatory role is consistent with the many examples of transcriptional regulation of T-beta-4 and of tissue-specific expression. Lymphocytes have a unique T-beta-4 transcript relative to the ubiquitous transcript found in many other tissues and cells. In a separate study, Clauss et al. (1991) stated that rat T-beta-4 is synthesized as a 44-amino acid propeptide which is processed into a 43-amino acid peptide by removal of the first methionyl residue and does not have a signal peptide. Comparison studies have shown that human T-beta-4 has a high degree of homology to rat T-beta-4; the coding regions differ by only 9 nucleotides, and these are all silent base changes.

Gondo et al. (1987) isolated a cDNA encoding T-beta-4 using differential screening of a cDNA library prepared from leukocytes of an acute lymphocytic leukemia patient. Utilizing Northern blot analysis, they studied the expression of the 830-nucleotide T-beta-4 mRNA in various primary myeloid and lymphoid malignant cell lines and in hemopoietic cell lines. Gondo et al. (1987) stated that the pattern of T-beta-4 gene expression suggests that it may be involved in an early phase of the host defense mechanism.

In other studies, Clauss et al. (1991) isolated a cDNA clone for the human interferon-inducible gene 6-26 (Friedman et al., 1984) and showed that its sequence was identical to that for the human T-beta-4. By use of a panel of human rodent somatic cell hybrids, Clauss et al. (1991) showed that the 6-26 cDNA recognized 7 genes, members of a multigene family, present on chromosomes 1, 2, 4, 9, 11, 20, and X. These genes are symbolized TMSL1, TMSL2, etc., respectively. Separately, Li et al. (1996) established that in the mouse there is a single Tmsb4 gene and that the lymphoid-specific transcript is generated by extending the ubiquitous exon 1 with an alternate downstream splice site. By interspecific backcross mapping, they located the mouse gene, which they symbolized Ptmb4, to the distal region of the mouse X chromosome, linked to Btk and Gja6. Thus, the human gene could be predicted to reside on the X chromosome in the general region of Xq21.3-q22, where BTK is located. By analysis of somatic cell hybrids, Lahn and Page (1997) mapped the T-beta-4, or TB4X, gene to the X chromosome. They noted that a homologous gene, TB4Y, is present on the Y chromosome.

Bao et al. (1996) found a novel member of the beta thymosin protein family expressed in a metastatic prostate carcinoma cell line. Prostate carcinoma is the most prevalent form of cancer in males and the second leading cause of cancer death among older males. The use of the serum prostate-specific antigen (PSA) test permits early detection of human prostate cancer; however, early detection has not been accompanied by an improvement in determining which tumors may progress to the metastatic stage. The process of tumor metastasis is a multistage event involving local invasion and destruction of extracellular matrix; intravasation into blood vessels, lymphatics or other channels of transport; survival in the circulation; extravasation out of the vessels into the secondary site; and growth in the new location. Common to many components of the metastatic process is the requirement for tumor cell motility. A well-characterized series of cell lines that showed varying metastatic potential was developed from the Dunning rat prostate carcinoma. Mohler et al. (1988) and Partin et al. (1989) showed a direct correlation between cell motility and metastatic potential in the Dunning cell lines. In studies comparing gene expression in poorly and highly motile metastatic cell lines derived from Dunning rat prostate carcinoma using differential mRNA display, Bao et al. (1996) found a novel member of the beta thymosin family of actin-binding molecules, named thymosin-beta-15 (T-beta-15), which was found to deregulate motility in prostate cells directly. In addition, it was expressed in advanced human prostate cancer specimens, but not in normal human prostate or benign prostatic hyperplasia, suggesting its potential use as a new marker for prostate carcinoma progression. Bao et al. (1996) also found that T-beta-15 levels correlated positively with the Gleason tumor grade. Coffey (1996) pointed out that the upregulation of T-beta-15 as a positive motility factor and the down regulation of the motility suppressor KAI1 provide the 'yin and yang' for metastasis; thus, he speculated that these pathways may provide a new target for therapy.

T-beta-4 has also been implicated in the acceleration of wound healing. Angiogenesis is an essential step in the repair process that occurs after injury. In our studies, we investigated whether the angiogenic thymic peptide, T-beta-4, enhanced wound healing in a rat full thickness wound model. Addition of T-beta-4 topically or intraperitoneally increased reepithelialization by 42% over saline controls at 4 d and by as much as 61% at 7 d post-wounding. Treated wounds also contracted at least 11% more than controls by day 7. Increased collagen deposition and angiogenesis were observed in the treated wounds. We also found that T-beta-4 stimulated keratinocyte migration in the Boyden chamber assay. After 4-5 h, migration

was stimulated 2-3-fold over migration with medium alone when as little as 10 pg of T-beta-4 was added to the assay. These results suggest that T-beta-4 is a potent wound healing factor with multiple activities that may be useful in the clinic.

The above defined information for this invention suggests that this beta thymosin-like protein may function as a member of a "beta thymosin family". Therefore, the novel nucleic acids and proteins identified here may be useful in potential therapeutic applications implicated in (but not limited to) various pathologies and disorders as indicated below. The potential therapeutic applications for this invention include, but are not limited to: protein therapeutic, small molecule drug target, antibody target (therapeutic, diagnostic, drug targeting/cytotoxic antibody), diagnostic and/or prognostic marker, gene therapy (gene delivery/gene ablation), research tools, tissue regeneration *in vivo* and *in vitro* of all tissues and cell types composing (but not limited to) those defined here.

The nucleic acids and proteins of the invention are useful in potential therapeutic applications implicated in cancer including but not limited to prostate cancer, immunological and autoimmune disorders (i.e. hyperthyroidism), angiogenesis and wound healing, modulation of apoptosis, neurodegenerative and neuropsychiatric disorders, age-related disorders, and other pathological disorders involving spleen, thymus, lung, and peritoneal macrophages and/or other pathologies and disorders. For example, a cDNA encoding the beta thymosin-like protein may be useful in gene therapy, and the beta thymosin-like protein may be useful when administered to a subject in need thereof. By way of nonlimiting example, the compositions of the present invention will have efficacy for treatment of patients suffering from cancer including but not limited to prostate cancer, immunological and autoimmune disorders (ie hyperthyroidism), angiogenesis and wound healing, modulation of apoptosis, neurodegenerative and neuropsychiatric disorders, age-related disorders, and other pathological disorders involving spleen, thymus, lung, and peritoneal macrophages. The novel nucleic acid encoding beta thymosin-like protein, and the beta thymosin-like protein of the invention, or fragments thereof, may further be useful in diagnostic applications, wherein the presence or amount of the nucleic acid or the protein are to be assessed. These materials are further useful in the generation of antibodies that bind immunospecifically to the novel substances of the invention for use in therapeutic or diagnostic methods.

The novel nucleic acid encoding the beta thymosin-like protein of the invention, or fragments thereof, may further be useful in diagnostic applications, wherein the presence or

amount of the nucleic acid or the protein are to be assessed. These materials are further useful in the generation of antibodies that bind immunospecifically to the novel substances of the invention for use in therapeutic or diagnostic methods. These antibodies may be generated according to methods known in the art, using prediction from hydrophobicity charts, as described in the “Anti-NOVX Antibodies” section below. The disclosed NOV2 proteins have multiple hydrophilic regions, each of which can be used as an immunogen. These novel proteins can be used in assay systems for functional analysis of various human disorders, which will help in understanding of pathology of the disease and development of new drug targets for various disorders.

10 NOV3

NOV3 includes two novel connexin-like proteins disclosed below. The disclosed proteins have been named NOV3a and NOV3b.

NOV3a

15 A novel nucleic acid was identified on chromosome 6 by TblastN using CuraGen Corporation’s sequence file for connexin or homolog as run against the Genomic Daily Files made available by GenBank or from files downloaded from the individual sequencing centers. The nucleic acid sequence was predicted from the genomic file Sequencing Center accession number: ba63k6_A by homology to a known connexin or homolog. Exons were predicted by
20 homology and the intron/exon boundaries were determined using standard genetic rules. Exons were further selected and refined by means of similarity determination using multiple BLAST (for example, tBlastN, BlastX, and BlastN) searches, and, in some instances, GeneScan and Grail. Expressed sequences from both public and proprietary databases were also added when available to further define and complete the gene sequence. The DNA sequence was then
25 manually corrected for apparent inconsistencies thereby obtaining the sequences encoding the full-length protein.

The novel nucleic acid of 1750 nucleotides (also referred to as GM_ba63k6_A) encoding a novel connexin-like protein is shown in Fig. 3A. An open reading frame was identified beginning with an ATG initiation codon at nucleotides 55-57 and ending with a TAA
30 codon at nucleotides 1684-1686. A putative untranslated region upstream from the initiation

codon and downstream from the termination codon is underlined in Fig. 3A, and the start and stop codons are in bold letters.

Table 3A. NOV3a Nucleotide Sequence (SEQ ID NO:9)

TGGGTGCTATTAACTCAGTGTTTTCTGTATATTTAGACATTAGTCTTTAA**CCAT**GGGGGACTGGAAC
TATTGGGTGGCATCCTAGAGGAAGTTCACCTCCCACTCAACCATAGTGGGGAAAATCTGGCTGACCATCTT
CTTCATCTTCCGAATGCTGGTACTTCGTGTGGCTGCTGAGGATGTCTGGGATGATGAACACTCAGCATTT
GCTGCACAACACCGGACGCCAGGTTGCAACATATCTGTTATGATGATGCATTCCTATCTCTTTGATCA
GGTTCCTGGGTTTTACAGATCATCTTTGTGTCTTCTCCTTCTTTGGTCTATATGGGCCATGCACTTTATA
GCTCAGGGCCTTTGAGAAAGACAGGCAGAGGAAAAAGTCACACCTTAGAGCCAGATGGAGAATCCAGAT
CTTGACTTGGAGGAGCAGCAAGAATAGATAGGGAAGCTGAGGAGGTTAGAGGAGCAGAAGAGGATCCATA
AAGTCCCCTCTGAAAGGATGTCTGCTGCGTACTTATGTCTTACACATCTTGACCAGATCTGTCTGGAAGT
AGGATTATGATAGGCCAATATATTTCTCTATGGGTTTCAAATGCAACCCCTTTACAAATGCATCAACCT
CCTTGCCCCAATGCGGTGGATTGCTTTGTATCTCAGGCCCACTGAGAAGACAATTTTCATGCTTTTTATGC
ACAGCATTGCAGCCATTTCTTGTACTCAATATACTGGAATATTTTCATCTAGGCATCAGAAAAATTAT
GAGGACACTTTATAAGAAATCCAGCAGTAGGGCATTGAGGATGAAACAGGCCCTCCATTCATTTGAAG
AAATATTCTGTGGCCAGCAGTGTATGATTTGCTCTTCTGCTGAAAGAAATCTCTCCACTTCAAGCTA
ACAATCAACAGCAAGCTATTCGAGTTAATGTGCCAAAGTCTAAACCATGTGGCAAATCCCACGCCAAG
GCAACTTGAAGTAGACCTTCCAATGGGAAAAGGACTGTCTGAGAAGGATCAGCAATAGCGGACAGCTC
CATGTTACAGCCCGTGTCCCTGGGCTGGCAGTGCTGGAATCAGCACCTGGGACAGCAATCAGACCATT
CCTCATTTGGCCTGCAGAATACAATGTCTCAGTCTCGGTAGGTACAACACGGCTCCTAGAAACTGTCC
ATCCTTTGACGTAGGAAGCTGGGAGCAGTCCAGGACAGACGAACCTCAGGTGAGCCTCTCACAGATCTT
CATAGTCACTGAGAGCAGTGAAGGCAGCATGAGGAGAGTGGGCTCGGATGACAGATCTCGCCAG
CAGTCGCAAGGCCAGCTTTCTGTCCAGATTGTTGTCTGAAAAGCGACATCTGCACAGTGACTCAGGAAG
CTCTGGTTCTCGGAATAGCTCCTGCTTGGATTTTCTCACTGGGAAAACAGCCCTCACCTCTGCCTTCA
GTCACTGGGCACAGAACATCAATGGTAAGACAGGCAGCCCTACCGATCATGGAACATACACAGAGCTGT
TCCATTCTGGATGCTTTTCTTTTCTTCTTCTTCTGGGCTGTGTATGTATGTTTGTGTTGACAGAGA
GCCAGATGGAGGGGAGATTTATTTAGGAGATAAAATTTATTCATGCATACATTCAGTTAAATTTCAAT
T**CATA**AAATAGACTAGAAAAATCTTATTATATCAATCGCTCTTATAAGTGCTGGGCATGTAATGGGTA

In a search of public sequence databases, it was found, for example, that the disclosed NOV3a nucleic acid sequence has 1274 of 1514 bases (84 %) identical to a *Mus musculus* connexin mRNA (GENBANK-ID: AJ010741)($E = 4.7e-245$). The nucleic acid also has 226 of 335 bases (67%) identical to a 1308 bp human gap junction protein alpha (GJA3) gene (GENBANK-ID:AF075290|acc:AF075290) ($E = 3.1e-36$). Public nucleotide databases include all GenBank databases and the GeneSeq patent database.

The disclosed NOV3a polypeptide (SEQ ID NO:10) encoded by SEQ ID NO:9 is 543 amino acid residues and is presented using the one-letter code in Table 3B. The NOV3a protein was analyzed for signal peptide prediction and cellular localization. SignalP, Psort and Hydropathy results predict that NOV3a has a signal peptide with most likely cleavage site pos. 41 and 42, at: VAA-ED, and that NOV3a is likely to be localized in the plasma membrane with a certainty of 0.6000.

Table 3B. Encoded NOV3a protein sequence (SEQ ID NO:10).

```

MGDWNLLGGILEEVHSHSTIVGKIWLTLFI FRMLVLRVAAEDVWDDEQSAFACNTRQPGCNNICYDDAFP
ISLIRFWVLQIIFVSSPSLVYMGHALYRLRAFEKDRQRKSHLRAQMENPDLDLEEQQRIDRELRRLEEOK
RIHKVPLKGCLLRTYVLHILTRSVLEVGFMIQYILYGFQMHPLYKCTQPPCPNAVDCFVSRPTEKTIFML
FMHSIAAISLLLNILEIFHLGIRKIMRTLYKKSSSEGIEDETGPPFHLKKYSVAQQCMICSSLPERISPLQ
ANNQQQVIRVNVPKSKTMWQIPQPRQLEVDPSNGKKDWSEKDKHSGQLHVHSPCPWAGSAGNQHLLGQQSDH
SSFGLQNTMSQSWLGTTTAPRNCPSFAVGTWEQSQDPEPSGEPLTDLHSHCRDSEGSMSRESGVWIDRSRPG
SRKASFLSRLLSEKRHLHSDSGSSGSRNSSCLDFPHWENSPSPLPSTGHRTSMVRQAALPIMELSQELFH
SGCFLFPFFLPGVCMYVCVDREADGGGDYLRDKIIHSIHSVKNFS

```

A BLASTX search was performed against public protein databases. The full amino acid sequence of the protein of the invention was found to have 393 of 485 amino acid residues (81%) identical to, and 422 of 485 residues (87%) positive with, the 505 amino acid residues connexin protein from *Mus musculus* (ptnr: SPTREMBL-ACC: Q9WUS4; E = 2.9e-211). The protein also has 138 of 258 residues (53%) identical to, and 188 of 258 residues (72%) positive with a 435 residue human gap junction protein (connexin) (SPTREMBL-ACC:Q9Y6H8; E = 2.8e-71)(Table 3C). The global sequence homology (as defined by GAP global sequence alignment with the full length sequence of this protein) is 84% amino acid similarity and 81% amino acid identity. In addition, this protein contains the connexin (IPR000500) protein domain (as defined by Interpro) at amino acid positions 1 to 233.

Table 3C. BLASTX results for NOV3a

Sequences producing High-scoring Segment Pairs:	Reading Frame	High Score	Smallest Sum Prob P (N)	N
ptnr:SPTREMBL-ACC:Q9WUS4 Connexin 57 - Mus musculus	+3	731	2.0e-71	1
ptnr:SPTREMBL-ACC:Q9Y6H8 Connexin - Homo Sapiens	+3	702	2.4e-68	1

NOV3b

In the present invention, the target sequence identified previously, Accession Number GMba63k6_A, was subjected to the exon linking process to confirm the sequence. PCR primers were designed by starting at the most upstream sequence available, for the forward primer, and at the most downstream sequence available for the reverse primer. In each case, the sequence was examined, walking inward from the respective termini toward the coding sequence, until a suitable sequence that is either unique or highly selective was encountered, or,

in the case of the reverse primer, until the stop codon was reached. Such primers were designed based on in silico predictions for the full length cDNA, part (one or more exons) of the DNA or protein sequence of the target sequence, or by translated homology of the predicted exons to closely related human sequences sequences from other species. These primers were then

5 employed in PCR amplification based on the following pool of human cDNAs: adrenal gland, bone marrow, brain - amygdala, brain - cerebellum, brain - hippocampus, brain - substantia nigra, brain - thalamus, brain -whole, fetal brain, fetal kidney, fetal liver, fetal lung, heart, kidney, lymphoma - Raji, mammary gland, pancreas, pituitary gland, placenta, prostate, salivary gland, skeletal muscle, small intestine, spinal cord, spleen, stomach, testis, thyroid,

10 trachea, uterus. Usually the resulting amplicons were gel purified, cloned and sequenced to high redundancy. The resulting sequences from all clones were assembled with themselves, with other fragments in CuraGen Corporation's database and with public ESTs. Fragments and ESTs were included as components for an assembly when the extent of their identity with another component of the assembly was at least 95% over 50 bp. In addition, sequence traces

15 were evaluated manually and edited for corrections if appropriate. These procedures provide the sequence reported below, which is designated Accession Number CG54734-02.

A disclosed NOV3b (also referred to as CG54734-02) nucleic acid of 1641 nucleotides is shown in Table 3D. An open reading frame was identified beginning with an ATG initiation codon at nucleotides 5-7 and ending with a TAA codon at nucleotides 1634-1636. A putative

20 untranslated region upstream from the initiation codon and downstream from the termination codon is underlined in Table 3D, and the start and stop codons are in bold letters.

Table 3D. NOV3b Nucleotide Sequence (SEQ ID NO:11)

TACCA**T**GGGGGACTGGAAC**T**TATGGGTGGCATCCTAGAGGAAG**T**CACTCCCACTCAACCATAGTGGGGA
 AAATCTGGCTGACCATCCTCTTCATCTTCCGAATGCTGGTACTTCGTGTGGCTGCTGAGGATGTCTGGGAT
 GATGAACAGTCAGCATTTGCCTGCAACACCCGGCAGGCAGGTTGCAACAATATCTGTTATGATGATGCATT
 CCCTATCTCTTTGATCAGGTTCTGGGTTTACAGATCATCTTTGTGTCTTCTCCTTCTTTGGTCTATATGG
 GCCATGCACTTTATAGGCTCAGGGCCTTTGAGAAAGACAGGCAGAGGAAAAAGTCACACCTTAGAGCCCAG
 ATGGAGAATCCAGATCTTGACTTGGAGGAGCAGCAAAGAATAGATAGGGAACTGAGGAGGTTAGAGGAGCA
 GAAGAGGATCCATAAAGTCCCTCTGAAAGGATGTCTGCTGCGTACTTATGTCTTACACATCTTGACCAGAT
 CTGTGCTGGAAGTAGGATTCATGATAGGCCAATATATCTCTATGGGTTTCAAATGCACCCCTTTACAAA
 TGCACTCAACCTCCTTGCCCCAATGCGGTGGATTGCTTTGTATCCAGGCCCACTGAGAAGACAATTTTCAT
 GCTTTTTATGCACAGCATTGCAGCCATTTCTTGTACTCAATATACTGGAAATATTTTCATCTAGGCATCA
 GAAAAATTATGAGGACACTTTATAAGAAATCCAGCAGTGAGGGCATTGAGGATGAAACAGGCCCTCCATTTC
 CATTTGAAGAAATATTCTGTGGCCAGCAGTGATGATTTGCTCTTCATTGCCTGAAAGAATCTCTCCACT
 TCAAGCTAACAAATCAACAGCAAGTCATTGAGTTAATGTGCCAAAGTCTAAAACCATGTGGCAATCCCAC
 AGCCAAGGCACTTGAAGTAGACCTTCCAATGGGAAAAAGGACTGGTCTGAGAAGGATCAGCATAGCGGA
 CAGCTCCATGTTACAGCCCGTGTCCCTGGGCTGGCAGTGCTGGAAATCAGCACCTGGGACAGCAATCAGA
 CCATTCTCATTTGGCCTGCAGAATACAATGTCTCAGTCCTGGCTAGGTACAACACGGCTCCTAGAAACT
 GTCCATCCTTTGCAGTAGGAACCTGGGAGCAGTCCCAGGACCCAGAACCCTCAGGTGAGCCTCTCACAGAT
 CTTCATAGTCACTGCAGAGACAATGAAGGCAGCATGAGAGAGAGTGGGGTCTGGATAGACAGATCTCGCCC

5

10

Table 3E. Encoded NOV3b protein sequence (SEQ ID NO:12).

15

Possible SNPs found for NOV3b are listed in Table 3F.

Table 3F: SNPs		
Consensus Position	Depth	Base Change
83	16	G>A
1242	21	A>G
1337	17	T>C

It was also found that NOV3a had homology to the amino acid sequences shown in the BLASTP data listed in Table 3G.

Table 3G. BLAST results for NOV3a					
Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
gi 14009611 gb AA K51676.1 AF296766 1 (AF296766)	connexin 62 [Homo sapiens]	543	508/543 (93%)	510/543 (93%)	0.0
gi 6753990 ref NP _034419.1	gap junction membrane channel protein alpha 10; connexin-57 [Mus musculus]	505	364/485 (75%)	394/485 (81%)	0.0
gi 10946367 gb AA G24878.1 (AF304048)	connexin 55.5 [Danio rerio]	498	170/277 (61%)	210/277 (75%)	1e-89
gi 13540537 ref N P_110399.1	connexin 59; gap junction alpha 10 [Homo sapiens]	515	161/246 (65%)	196/246 (79%)	2e-88
gi 12719964 ref X P_001660.2	gap junction protein, alpha 8, 50kD (connexin 50) [Homo sapiens]	433	128/245 (52%)	167/245 (67%)	4e-66

The homology of these sequences is shown graphically in the ClustalW analysis shown in Table 3H.

Table 3H. ClustalW Analysis of NOV3a

- 1) Novel NOV3a (SEQ ID NO:10)
- 2) gi|14009611|gb|AAK51676.1| connexin 62 [Homo sapiens] (SEQ ID NO:44)
- 3) gi|6753990|ref|NP_034419.1| gap junction membrane channel protein alpha 10; connexin-57 [Mus musculus] (SEQ ID NO:45)
- 4) gi|10946367|gb|AAG24878.1| connexin 55.5 [Danio rerio] (SEQ ID NO:46)
- 5) gi|13540537|ref|NP_110399.1| connexin 59; gap junction alpha 10 [Homo sapiens] (SEQ ID NO:47)
- 6) gi|12719964|ref|XP_001660.2| gap junction protein, alpha 8, 50kD (connexin 50) [Homo sapiens] (SEQ ID NO:48)

[illegible]

		430	440	450	460	470	480
5	NOV3A	G---SMRESGVWIDFSRPGSRKASFLSRLSEKRRH-----LHSDSGSSGSRNSSCLDFP					
	gi 14009611	G---SMRESGVWIDFSRPGSRKASFLSRLSEKRRH-----LHSDSGSSGSRNSSCLDFP					
	gi 6753990	G---SARESGVWTDRLGPGSRKASFLSRLSEKRRH-----LHSDSGSSGSRNSSCLDFP					
	gi 10946367	-----HASSSMVKKPKWKSAPWNCSTVVEGNGSDSDSLEGSKARCPYSAVARTSSRSD--					
	gi 13540537	QTVFSLPANCWKKPRWLRATWGSSTEHENRGSPPK--GNLKGQFRKCTVETLPPSQGDS-					
10	gi 12719964	E---EQEKVAVPE-----GEKVETPGVDKEGEKEE-----PQSEKVSQKQGLP-----					
		490	500	510	520	530	540
15	NOV3A	HWENSPSPPLPSVTGHRIS--MVRRAALFIMELSQELFHSGCCLEPFFFLPGVCMYVCVDRE					
	gi 14009611	HWENSPSPPLPSVTGHRIS--MVRRAALFIMELSQELFHSGCCLEPFFFLPGVCMYVCVDRE					
	gi 6753990	HWENSPSPPLPSVTGHRIS--MVRRAALFIMELSQELFHSGCCLEPFFFLPGVCMYVCVDRE					
	gi 10946367	HWENSPSPPLPSATGHRAS--MVRRAALFIMELSQELFHSGCCLEPFFFLPGVCMYVCVDRE					
	gi 13540537	TKLSRPTSPDSVEESSSE-----SRHSERASPSHRASLASSSSSRRAAPTDLQI-----					
	gi 12719964	QSLDIPNTADSLGCLSFEPGLVRTCNNVCPENHIVSLTNNLLG-RRVPTDLQI-----					
20		-AEKTPSLCPELTDDAR-----PLSRLSKASSRAR--S-DLITV-----					
		550	560				
25	NOV3A	ADGGGDYLWRDKIIHSIHSVKNFS					
	gi 14009611	ADGGGDYLWRDKIIHSIHSVKNFS					
	gi 6753990	-----					
	gi 10946367	-----					
	gi 13540537	-----					
	gi 12719964	-----					

The homologies shown above are shared by NOV3b insofar as NOV3b and NOV3a are homologous.

Tables 3I and 3J list the domain description from DOMAIN analysis results against NOV3a. This indicates that the NOV3a sequence has properties similar to those of other proteins known to contain this domain.

Table 3I. Domain Analysis of NOV3a

gnl|Smart|CNX, Connexin homologues (SEQ ID NO:49)
CD-Length = 34 residues, 100.0% aligned
Score = 63.5 bits (153), Expect = 3e-11

		10	20	30
35	NOV3A	DVWDDDEQSAFACNTRQPGCENNYCYDDAFPISLIR		
40	Smart_CNX	DVWGDDEQSDDFVCNTOQPGCENVCYDHHFFPISHIR		

Table 3J. Domain Analysis of NOV3a

gnl|Pfam|pfam00029, connexin, Connexin. (SEQ ID NO:50)
CD-Length = 218 residues, 91.3% aligned
Score = 284 bits (726), Expect = 1e-77

		10	20	30	40	50	60
45	NOV3A	MCDWNLLCGTILEVHSHSTIVGKIWLITLFIIFRMLVLRVAAE DVWDDDEQSAFACNTRQPG					
	Pfam_pfam00029	M-DWSFLGRLLLEGVNEHSTAGKRWLSVLFIFRMLVLRVAAE SVWGDDEQSDDFVCNTOQPG					

		70	80	90	100	110	120	
NOV3A							
Pfam_pfam00029							
5		NOV3A	CNNIC	YDDA	FPISL	TFWV	LQIIFVSSPSLV	YMGHALYRLRAFERDRORKKS-----HLR
		Pfam_pfam00029	CENV	YCDQ	FPISH	VMRL	NVLQIIFVSTPSLL	YLGHVAYRVKKEKKEKEKEE-----Q--
							
10		NOV3A	AQMEN	PDLDLE	EQOR	IDREL	R-----RLEE	QKRTHKVP
		Pfam_pfam00029	---SKS	LYTR	ECKK	-----Q-----	ARDE	TGKVR---TRG
							
15		NOV3A	CILRT	YVLH	ILTR	SVLEV	GFMIGQY	ILY-GFQMHPLYKCTQP-PCPN
		Pfam_pfam00029	GLWR	TYVFS	ITFK	TFEV	GFLYGOY	LLY-GFTLSPLVVC
							
20		NOV3A	LEML	FMH	STA	ATSL	LLNLE	IFHL
		Pfam_pfam00029	IFIV	FML	VSA	ICLL	LNLA	EYHL
							
			250	260				

The connexins are a family of integral membrane proteins that oligomerise to form intercellular channels that are clustered at gap junctions. These channels are specialized sites of cell-cell contact that allow the passage of ions, intracellular metabolites and messenger molecules (with molecular weights of 1-2 kD) from the cytoplasm of one cell to its apposing neighbors. They are found in almost all vertebrate cell types, and somewhat similar proteins have been cloned from plant species. Invertebrates utilize a different family of molecules, innexins that share a similar predicted secondary structure to the vertebrate connexins, but have no sequence identity to them.

Vertebrate gap junction channels are thought to participate in diverse biological functions. For instance, in the heart they permit the rapid cell-cell transfer of action potentials, ensuring coordinated contraction of the cardiomyocytes. They are also responsible for neurotransmission at specialized 'electrical' synapses. In non-excitable tissues, such as the liver, they may allow metabolic cooperation between cells. In the brain, gap junctions extensively couples glial cells; this allows waves of intracellular Ca^{2+} to propagate through nervous tissue, and may contribute to their ability to spatially-buffer local changes in extracellular K^{+} concentration.

The connexin protein family is encoded by at least 13 genes in rodents, with many homologues cloned from other species. They show overlapping tissue expression patterns, most tissues expressing more than one connexin type. Their conductances, permeability to different molecules, phosphorylation and voltage-dependence of their gating, have been found to vary. Possible communication diversity is increased further by the fact that gap junctions may be

formed by the association of different connexin isoforms from apposing cells. However, in vitro studies have shown that not all possible combinations of connexins produce active channels.

Hydropathy analysis predicts that all cloned connexins share a common transmembrane (TM) topology. Each connexin is thought to contain 4 TM domains, with two extracellular and three cytoplasmic regions. This model has been validated for several of the family members by in vitro biochemical analysis. Both N- and C-termini are thought to face the cytoplasm, and the third TM domain has an amphipathic character, suggesting that it contributes to the lining of the formed-channel. Amino acid sequence identity between the isoforms is ~50-80%, with the TM domains being well conserved. Both extracellular loops contain characteristically conserved cysteine residues, which likely form intramolecular disulphide bonds. By contrast, the single putative intracellular loop (between TM domains 2 and 3) and the cytoplasmic C-terminus are highly variable among the family members. Six connexins are thought to associate to form a hemi-channel, or connexon. Two connexons then interact (likely via the extracellular loops of their connexins) to form the complete gap junction channel.

Gap junctions were first characterized by electron microscopy as regionally specialized structures on plasma membranes of contacting adherent cells. These structures were shown to consist of cell-to-cell channels. Connexin proteins are purified from fractions of enriched gap junctions from different tissues differ. The connexins are designated by their molecular mass. Another system of nomenclature divides gap junction proteins into 2 categories, alpha and beta, according to sequence similarities at the nucleotide and amino acid levels. For example, CX43 is designated alpha-1 gap junction protein, whereas CX32 and CX26 are called beta-1 and beta-2 gap junction proteins, respectively. This nomenclature emphasizes that CX32 and CX26 are more homologous to each other than either of them is to CX43.

Willecke et al. (1990) used rat connexin gene probes in Southern blot analysis of human-mouse somatic cell hybrids to map the CX26 gene to chromosome 13. By means of somatic cell hybrids, Hsieh et al. (1991) assigned the GJB2 gene to chromosome 13 in man and chromosome 14 in the mouse. Haefliger et al. (1992) showed that the rat homologs of the CX26 and CX46 genes are tightly linked on chromosome 14. By isotopic in situ hybridization, Mignon et al. (1996) mapped GJB2 to 13q11-q12 and confirmed the assignment to mouse chromosome 14.

Various studies have been carried out to investigate the role(s) of altered genes or proteins from the connexin family. Kelsell et al. (1997) studied a pedigree containing

individuals with autosomal dominant deafness and identified a mutation in the CX26 gene: a101T-C transition resulting in a met34-to-thr amino acid substitution. CX26 mutations resulting in premature stop codons were also found in 3 autosomal recessive nonsyndromic sensorineural deafness pedigrees, genetically linked to 13q11-q12, where the CX26 gene is localized. Immunohistochemical staining of human cochlear cells for CX26 demonstrated high levels of expression. Kelley et al. (1998) presented evidence that the 101T-C missense mutation identified by Kelsell et al. (1997) in individuals with autosomal dominant nonsyndromic deafness is not sufficient to cause hearing loss.

Carrasquillo et al. (1997) performed linkage analysis in 2 interrelated inbred kindreds in a single Israeli-Arab village containing more than 50 individuals with nonsyndromic recessive deafness. Genetic mapping demonstrated that a gene located at 13q11 (DFNB1) segregated with the deafness in these 2 kindreds. Haplotype analysis, using 8 microsatellite markers spanning 15 cM in 13q11, suggested the segregation of 2 different mutations in this extended kindred; affected individuals were homozygotes for either haplotype or compound heterozygotes. Carrasquillo et al. (1997) identified 2 distinct mutations, trp77 to arg and 35delG, in the CX26 gene, both of which were predicted to inactivate connexin 26. The recombination of marker alleles involving polymorphisms in 13q11, at known map distances from the mutations, allowed them to estimate the age of the mutations to be 3 to 5 generations (75 to 125 years). The study demonstrated that in small populations with high rates of consanguinity, as compared with large outbred populations, recessive mutations may have very recent origin and show allelic diversity. They pointed to the same phenomenon being observed for Hurler syndrome with 3 unique mutations and for metachromatic leukodystrophy with 5 distinct mutations, discovered among the Druze and Muslim Arab villages in Israel. In light of these findings, the authors commented that it is likely that homozygosity mapping studies in highly inbred communities may be compromised, as may be studies of mapping by linkage disequilibrium, unless the possibility of mutational diversity is taken into account.

Lench et al. (1998) studied the role of CX26 mutations in singleton (sporadic) cases of nonsyndromal sensorineural deafness. Such mutations were identified in 4 of 43 U.K. and 2 of 25 Belgian patients. Thus, about 10% of families presenting with a child sporadically affected with this disorder can be offered definitive mendelian recurrence risks. This was said to be the first genetic test available for screening such children.

Kelley et al. (1998) analyzed 58 multiplex families each having at least 2 affected children diagnosed with autosomal recessive nonsyndromic deafness. Mutations in both alleles of GJB2 were observed in 20 of the 58 families. A 30delG allele occurred in 33 of the 116 chromosomes, for a frequency of 0.284. This mutation was observed in 2 of 192 control chromosomes, for an estimated gene frequency of 0.01 ± 0.007 . The homozygous frequency of the 30delG allele was then estimated at 0.0001, or 1 in 10,000. Given that the frequency of all childhood hearing impairment is 1 in 1,000 and that half of that is genetic, the specific mutation 30delG is responsible for 10% of all childhood hearing loss and for 20% of all childhood hereditary hearing loss. Six novel mutations were also observed in the affected population.

In more recent studies, Murgia et al. (1999) studied 53 unrelated individuals with non syndromic sensorineural hearing impairment and carried out CX26 mutation analysis. Mutations were found in 53% of cases, in 35.3% of those in whom autosomal recessive inheritance was thought likely and in 60% of the presumed sporadic cases. Three novel mutations were found. The hearing deficit varied from mild to profound even within the same family. Among patients with profound hearing loss, 35.5% were found to have a mutation; among those severely impaired, 20%; and among those moderately impaired, 33.3%. Rabionet et al. (2000) analyzed the GJB2 gene in 576 families/unrelated patients with recessive or sporadic deafness from Italy and Spain, 193 of them being referred as autosomal recessive and the other 383 as apparently sporadic. Of the 1,152 unrelated GJB2 chromosomes, 37% had GJB2 mutations. A total of 23 different mutations were detected. Mutation 35delG was the most common, accounting for 82% of all GJB2 deafness alleles. It represented 88% of the alleles in Italian patients and only 55% in Spanish cases. Sobe et al. (2000) sequenced the entire coding region of the GJB2 gene in 75 hearing-impaired children and adults in Israel. Age at onset in the screened population was both prelingual and postlingual, with hearing loss ranging from moderate to profound. Almost 39% of all persons tested harbored GJB2 mutations, most of which were 35delG and 167delT. A novel mutation, involving both a deletion and an insertion, 51del12insA, was identified in a family originating from Uzbekistan. All GJB2 mutations were associated with prelingual hearing loss, although severity ranged from moderate to profound, with variability even among hearing-impaired sibs. No significant difference in hearing levels was found between individuals with 35delG and 167delT mutations.

The above defined information for this invention suggests that these connexin-like protein (NOV3a and 3b) may function as members of the “connexin family”. Therefore, the novel nucleic acids and proteins identified here may be useful in potential therapeutic applications implicated in (but not limited to) various pathologies and disorders as indicated below. The potential therapeutic applications for this invention include, but are not limited to: protein therapeutic, small molecule drug target, antibody target (therapeutic, diagnostic, drug targeting/cytotoxic antibody), diagnostic and/or prognostic marker, gene therapy (gene delivery/gene ablation), research tools, tissue regeneration *in vivo* and *in vitro* of all tissues and cell types composing (but not limited to) those defined here.

The nucleic acids and proteins of the invention are useful in potential therapeutic applications implicated in mutilating palmoplantar keratoderma (PPK), X-linked Charcot-Marie-Tooth neuropathy, hereditary peripheral neuropathy, hereditary non-syndromic sensorineural deafness, vohwinkel's syndrome an autosomal dominant disease characterized by hyperkeratosis, constriction on finger and toes and congenital deafness and other pathologies and disorders. For example, a cDNA encoding the connexin-like protein may be useful in gene therapy, and the connexin-like protein may be useful when administered to a subject in need thereof. By way of nonlimiting example, the compositions of the present invention will have efficacy for treatment of patients suffering from Clouston syndrome and deafness, mutilating palmoplantar keratoderma (PPK), X-linked Charcot-Marie-Tooth neuropathy, hereditary peripheral neuropathy. The novel nucleic acid encoding connexin-like protein, and the connexin-like protein of the invention, or fragments thereof, may further be useful in diagnostic applications, wherein the presence or amount of the nucleic acid or the protein are to be assessed. These materials are further useful in the generation of antibodies that bind immunospecifically to the novel substances of the invention for use in therapeutic or diagnostic methods.

The novel nucleic acids encoding the connexin-like proteins of the invention, or fragments thereof, may further be useful in diagnostic applications, wherein the presence or amount of the nucleic acid or the protein are to be assessed. These materials are further useful in the generation of antibodies that bind immunospecifically to the novel substances of the invention for use in therapeutic or diagnostic methods. These antibodies may be generated according to methods known in the art, using prediction from hydrophobicity charts, as described in the “Anti-NOVX Antibodies” section below. The disclosed NOV3 proteins have

multiple hydrophilic regions, each of which can be used as an immunogen. In one embodiment, a contemplated NOV3 epitope is from about amino acids 40 to 70. In another embodiment, a NOV3 epitope is from about amino acids 85 to 145. In additional embodiments, NOV3 epitopes are from about amino acids 175 to 200, 225-270, 280-480 and from about amino acids 510 to 530. These novel proteins can be used in assay systems for functional analysis of various human disorders, which will help in understanding of pathology of the disease and development of new drug targets for various disorders.

NOV4

NOV4 includes four novel hepatoma derived growth factor-like proteins disclosed below. The disclosed proteins have been named NOV4a, NOV4b, NOV4c and NOV4d.

NOV4a

A novel nucleic acid of 2031 nucleotides (also referred to as 85731808_EXT) encoding a novel Hepatoma Derived Growth Factor-like protein is shown in Fig. 4A. An open reading frame was identified beginning with an ATG initiation codon at nucleotides 1-3 and ending with a TGA codon at nucleotides 2029-2031. The start and stop codons are in bold letters in Fig. 4A.

Table 4A. NOV4a Nucleotide Sequence (SEQ ID NO:13).

<p>ATGCCAAACGCCTTTAAACCCGGGGACTTGGTTTTCCCTAAAATTAAGGGCTACCCTCAATGGCCTTCCAG GATCGACGACATCGCGGATGGCGCCGTGAAGCCCCACCAACAAGTACCCCATCTTTTCTTTGGCACAC ACGAAACGGCCTTCCTGGGACCCAAGGACCTGTTCCCTACGACAAATGTAAAGACAAGTACGGGAAGCCC AACAAGAGGAAAGGCTTCAATGAAGGGCTGTGGGAGATCCAGAACAACCCACGCCAGCTACAGCGCCCC TCCGCCAGTGAGCTCCTCCGACAGCGAGGCCCCGAGGCCAACCCGCCGACGGCAGTGACGCTGACGAGG ACGATGAGGACCGGGGGTCAATGGCCGTACAGCGGTAACCGCCACAGCTGCCAGCGACAGGATGGAGAGC GACTCAGACTCAGACAAGAGTAGCGACAACAGTGGCCTGAAGAGGAAGACGCCTGCGCTAAAGGTATCGGT CTCGAAACGAGCCGAAAGGCCTCCAGCGACCTGGATCAGGCCAGCGTGTCCCATCCGAAGAGGAGAACT CGGAAAGCTCATCTGAGTCGGAGAAGACCAGCGACCAGGACTTCACACCTGAGAAGAAAGCAGCGGTCCGG GCGCCACGGAGGGGCCCTCTGGGGGACGGAAAAAAGAAGGCGCCATCAGCCTCCGACTCCGACTCCAA GGCCGATTTCGGACGGGGCCAAGCCTGAGCCGGTGGCCATGGCGCGGTCCGCGTCTCTCTCTCTCTCT CCTCTCTCTCCGACTCCGATGTGTCTGTGAAGAAGCCTCCGAGGGGACGGAAGCCAGCGGAGAAGCCTCTC CCGAAGCCGCGAGGGCGGAAACCGAAGCCTGAACGGCTCCGTCCAGCTCCAGCAGTGACAGTGACAGCGA CGAGGTGGACCGCATCAGTGAGTGGGAAGCGGCGGGACGAGGCGCGGAGGCGGAGCTGGAGGCCCGCGGC GGCGAGAGCAGGAGGAGGAGCTGCGGCGCCTGCGGGAGCAGGAGAAGGAGGAGAAGGAGCGGAGGCGCGAG CGGGCCGACCGCGGGGAGGCTGAGCGGGGACGCGCGGACGAGCTCAGGGAGGACGATGA GCCCGTCAAGAAGCGGGACGCAAGGGCCGGGGCCGGGTCCCCGTCTCTCTGACTCCGAGCCGAGG CCGAGCTGGAGAGAGAGGCCAAGAAATCAGCGAAGAAGCGCAGTCTCAAGCACAGAGCCCGCCAGGAAA CCTGGCCAGAAGGAGAAGAGAGTGGCGCCGAGGAGAAGCAACAAGCCAGGCCGTGAAGGTGGAGCGGAC CCGGAAGCGGTCCGAGGGCTTCTCGATGGACAGGAAGGTAGAGAAGAAGAAAGAGCCCTCCGTGGAGGAGA AGCTGCAGAAGCTGCACAGTGAGATCAAGTTTGCCCTAAAGGTGCACAGCCCGGACGTGAAGAGGTGCCTG AATGCCCTAGAGGAGCTGGGAACCTGCAGGTGACCTCTCAGATCCTCCAGAAGAACACAGACGTGGTGGC CACCTTGAAGAAGATTGCGCGTTACAAAGCGAACAAGGACGTAATGGAGAAGGCAGCAGAAGTCTATACCC GGCTCAAGTCGCGGGTCTCTCGGCCAAAGATCGAGGCGGTGCAGAAAGTGAACAAGGCTGGGATGGAGAAG</p>

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GAGAAGGCCGAGGAGAAGCTGGCCGGGGAGGAGCTGGCCGGGGAGGAGCTGGCCGGGGAGGAGGCCCCCA
GGAGAAGGCCGAGGACAAGCCCAGCACCGATCTCTCAGCCCCAGTGAATGGCGAGGCCACATCACAGAAGG
GGGAGAGCGCAGAGGACAAGGAGCACGAGGAGGGTCTGGGACTCGGAGGAGGGGCCAAGGTGTGGCTCCTCT
GAAGACCTGCACGAGAGCGTACGGGAGGGTCCCCACCTGGACAGGCCTGGGAGCGACCGGCAGGAGCGCGA
GAGGGCACGGGGGGACTCGGAGGCCCTGGACGAGGAGAGCTGA

```

In a search of public sequence databases, it was found, for example, that the nucleic acid sequence (NOV4a) has 1268 of 1775 bases (71%) identical to a *Mus musculus* Hepatoma Derived Growth Factor-like protein mRNA (GENBANK-ID:D63850) ($E = 2.5 \times 10^{-174}$). It is also 70% similar over 364 bp to a separate, but partially overlapping, fragment of the same gene.

The NOV4a polypeptide (SEQ ID NO:14) encoded by SEQ ID NO:13 is 676 amino acid residues and is presented using the one-letter amino acid code in Table 4B. The NOV4a protein was analyzed for signal peptide prediction and cellular localization. SignalP, Psort and Hydropathy profile indicate that NOV4a does not have a signal peptide and is likely to be localized in the nucleus with a certainty of 0.9866. However, the protein predicted here is similar to the "Hepatoma Derived Growth Factor-Like Protein Family", some members of which end up outside the cell and exhibit growth factor activity. Therefore it is likely that NOV4a is available at the appropriate sub-cellular localization and hence accessible for the therapeutic uses described in this application.

Table 4B. NOV4a protein sequence (SEQ ID NO:14)

```

MPNAFKPGDLVFPKIKGYFPQWPSRIDDIADGAVKPPPNKYPIFFFGTHETAFLGPKDLFPYDKCKDKYGKPNKR
KGFNEGLWEIQNNPHASYSAPPPVSSSDSEAPEANPADGSDADEDDRGVMAVTAVTATAASDRMESDSDSDK
SSDNSGLKRKTPALKVSVSKRARKASSDLQASVSPSEEEENSESSSESEKTSDDQFTPEKKA AVRAPRRGPLGG
RKKKKAPSASDSDSKADSDGAKPEPVAMARSASSSSSSSSSSSDSVSVKKPPRGRKPAEKPLPKPRGRKPKPER
PPSSSSSDSDSDEVDRISEWKRRDEARRRELEARRRREQEELRRLREQEKEEKERRRERADRGEAERGSGGSS
GDELREDDEPVKKRGRKGRGRGPPSSDSEPEAELEAEAKSAKKPQSSSTEPARKPGQKEKVRPEEKQQARP
VKVERTKRKSEGFMSMDRKVEKKKEPSVEEKLQKLHSEIKFALKVDSPDVKRCLNALEELGTLQVTSQILQKNTD
VVATLKKIRRYKANKDVMKAAEVYTRLKSRVLGPKIEAVQKVNKAGMEKEKAEKLAGEEELAGEELAGEEAPQ
EKAEDKPFSTDL SAPVNGEATSQKGE SAEDKEHEEGRDSEEGPRCGSSEDLHESVREGPDLD RPSDRQERERAR
GDSEALDEES

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The Hepatoma Derived Growth Factor-like protein (NOV4a) maps to chromosome 19 and is expressed in at least the following tissues: lung, blood, lymphocyte, bone marrow, colon, brain, pancreas, pituitary, testis, ovaries, prostate, and uterus.

The full amino acid sequence of the NOV4a protein was found to have 548 of 676 amino acid residues (81%) identical to, and 601 of 676 residues (88%) similar to, the 669

amino acid residue Hepatoma Derived Growth Factor-like protein from *Mus musculus* (SPTREMBL-ACC:O35540; E= 1.3 e-284) (Table 4C).

Table 4C. BLASTX results for NOV4a					
Sequences producing High-scoring Segment Pairs:		Reading Frame	High Score	Smallest Sum Prob P(N)	N
ptnr:SPTREMBL-ACC:O35540 Hepatoma-Derived GF - Mus		+1	2742	1.3e-284	1

NOV4a, as well as 4b, 4c and 4d, sequences were initially identified by searching a proprietary sequence file database for DNA sequences which translate into proteins with similarity to Hepatoma Derived Growth Factor-Like Proteins. NOV4a was identified as having suitable similarity. NOV4a was analyzed further to identify any open reading frames encoding novel full length proteins as well as novel splice forms of these genes. This was done by extending the identified NOV4a using suitable sequences from additional proprietary assemblies, publicly available EST sequences and public genomic sequences. A Genomic clone (AC011498) HTG Homo sapiens chromosome 19 clone CTB-50L17 was identified as having regions with 100% identity to the NOV4a and was selected for analysis because this identity implied that this clone contained the sequence of the genomic locus for NOV4a.

The genomic clone was analysed by Genscan and Grail to identify exons and putative coding sequences/open reading frames. This clone was also analyzed by TblastN, BlastX and other homology programs to identify regions translating to proteins with similarity to the original protein/protein family of interest. Expressed sequences from both public and proprietary databases were also added when available to further define and complete the gene sequence. The DNA sequence was then manually corrected for apparent inconsistencies thereby obtaining the sequences encoding the full-length protein.

NOV4b

In the present invention, the target sequence identified above, Accession Number 85731808_EXT, was subjected to the exon linking process to confirm the sequence. PCR primers were designed by starting at the most upstream sequence available, for the forward primer, and at the most downstream sequence available for the reverse primer. In each case, the sequence was examined, walking inward from the respective termini toward the coding

sequence, until a suitable sequence that is either unique or highly selective was encountered, or, in the case of the reverse primer, until the stop codon was reached. Such suitable sequences were then employed as the forward and reverse primers in a PCR amplification based on a library containing a wide range of cDNA species. The resulting amplicon was gel purified, cloned and sequenced to high redundancy to provide the sequence reported below, which is designated Accession Number 21143463.0.45.

A disclosed NOV4b (also referred to as 21143463.0.45) nucleic acid of 2004 nucleotides is shown in Fig. 4D. An open reading frame was identified beginning with an ATG initiation codon at nucleotides 1-3 and ending with a TGA codon at nucleotides 2002-2004.

The start and stop codons are in bold letters in Fig. 4D.

Table 4D. NOV4b Nucleotide Sequence (SEQ ID NO:15).

ATGCCACACGCCTTCAAGCCCGGGGACTTGGTGTTCGCTAAGATGAAGGGCTACCCTCACTGGCCTGCCAG
GGTGGACGACATCGCGGATGGCGCCGTGAAGCCCCACCAACAAGTACCCCATCTTTTTCTTTGGCACAC
ACGAAACGGCCTTCTGGGACCCAAGGACCTGTTCCCTACGACAAATGTAAAGACAAGTACGGGAAGCCC
AACAAGAGGAAAGGCTTCAATGAAGGGCTGTGGGAGATCCAGAACAACCCCCACGCCAGCTACAGCGCCCC
TCCGCCAGTGAGCTCCTCCGACAGCGAGGCCCCGAGGCCAACCCCGCCGACGGCAGTGACGCTGACGAGG
ACGATGAGGACCGGGGGTTCATGGCCGTACAGCGGTAACCGCCACAGCTGCCAGCGACAGGATGGAGAGC
GACTCAGACTCAGACAAGAGTAGCGACAACAGTGGCCTGAAGAGGAAGACGCCTGCGCTAAAGGTATCGGT
CTCGAAACGAGCCGAAAGGCCTCCAGCGACCTGGATCAGGCCAGCGTGTCCCATCCGAAGAGGAGAACT
CGGAAAGCTCATCTGAGTCGGAGAAGACCAGCGACCAAGGACTTCACACCTGAGAAGAAAGCAGCGGTCCGG
GCGCCACGGAGGGGCCCTCTGGGGGACGGAAAAAAGAAGGCGCCATCAGCCTCCGACTCCGACTCCAA
GGCCGATTTCGACGGGGCCAAGCCTGAGCCGCTGGCCATGGCGCGGTCCGCGTCTCTCTCTCTCTCTCT
CCTCTCTCTCCGACTCCGATGTGTCTGTGAAGAAGCCTCCGAGGGGACAGGAAGCCAGCGGAGAAGCCTCTC
CCGAAGCCGCGAGGGCGGAAACCGAAGCCTGAACGGCCTCCGTCCAGCTCCAGCAGTGACAGTGACAGCGA
CGAGGTGGACCGCATCAGTGAGTGGAAGCGGCGGGACGAGGCGCGGAGGCGGAGCTGGAGGCCCGGCGGC
GGCGAGAGCAGGAGGAGGAGCTGCGGCGCCTGCGGGAGCAGGAGAAGGAGGAGAAGGAGCGGAGGCGCGAG
CGGGCCGCTGAGCGGGGCAGCGGCGGCAGCAGCGGGGACGAGCTCAGGGAGGACGATGAGCCCGTCAAGAA
GCGGGGACGCAAGGGCCGGGGCCGGGGTCCCCCGTCTCTCTGACTCCGAGCCCGAGGCCGAGCTGGAGA
GAGAGGCCAAGAAATCAGCGAAGAAGCCGAGTCTCAAGCACAGAGCCCGCCAGGAAACCTGGCCAGAAG
GAGAAGAGAGTGCGGCCCCGAGGAGAAGCAACAAGCCAAGCCGTGAAGGTGGAGCGGACCCGGAAGCGGTC
CGAGGGCTTCTCGATGGACAGGAAGGTAGAGAAGAAGAAGAGCCCTCCGTGGAGGAGAAGCTGCAGAAGC
TGCACAGTGAGATCAAGTTTGGCCTAAAGGTCGACAGCCCGACGTGAAGAGGTGCCTGAATGCCCTAGAG
GAGCTGGGAACCTGCAGGTGACCTCTCAGATCCTCCAGAAGAACACAGACGTGGTGGCCACCTTGAAGAA
GATTTCGCGTTACAAAGCGAACAAGGACGTAATGGAGAAGGCAGCAGAAGTCTATACCCGGCTCAAGTCGC
GGGTCTCGGCCCAAGATCGAGGCGGTGCAGAAAGTGGACAAGGCTGGGATGGAGAAGGAGAAGGCCGAG
GAGAAGCTGGCCGGGAGGAGCTGGCCGGGGAGGAGGCCCCCAGGAGAAGGCGGAGGACAAGCCCAGCAC
CGATCTCTCAGCCCCAGTGAATGGCGAGGCCACATCACAGAAGGGGGAGAGCGCAGAGGACAAGGAGCACG
AGGAGGGTCTGGGACTCGGAGGAGGGGCCAAGGTGTGGCTCCTCTGAAGACCTGCACGAGAGCGTACGGGAG
GGTCCCGACCTGGACAGGCCTGGGAGCGACCGGCAGGAGCGCAGAGGGCACGGGGGACTCGGAGGCCCT
GGACGAGGAGAGCTGA

The NOV4b polypeptide (SEQ ID NO:16) encoded by SEQ ID NO:15 is 667 amino acid residues and is presented using the one-letter amino acid code in Table 4E. The NOV4b protein was analyzed for signal peptide prediction and cellular localization. SignalP, Psort and Hydropathy profile indicate that NOV4b does not have a signal peptide and is likely to be localized in the nucleus with a certainty of 0.9867. However, the protein predicted here is

similar to the "Hepatoma Derived Growth Factor-Like Protein Family", some members of which end up outside the cell and exhibit growth factor activity. Therefore it is likely that NOV4b is available at the appropriate sub-cellular localization and hence accessible for the therapeutic uses described in this application. NOV4b has a molecular weight of 73827.3 Daltons.

Table 4E. NOV4b protein sequence (SEQ ID NO:16)

MPHAFKPGDLVFAKMGYPHWPARVDDIADGAVKPPPNKYPIFFFGTHETAFLGPKDLFPYDKCKDKYGKPNKR
KGFNEGLWEIQNNPHASYSAPPPVSSSDSEAPEANPADGSDADEDDDRGVMVAVTAVTATAASDRMESDSDSDK
SSDNSGLKRRKTPALKVSVSKRARKASSDLQASVSPSEEEENSESSSESEKTSDDQDFTPEKKA AVRAPRRGPLGG
RKKKKAPSASDSDSKADSDGAKPEPVAMARSASSSSSSSSSSSDSDSVSVKKPPRGRKPAEKPLPKPRGRKPKPER
PPSSSSSDSDSDEVDRISEWKRRDEARRRELEARRRREQEELRRLREQEKEEKERRRERAAERGS GGSSGDEL
REDDEPVKKRGRKGRGRGPPSSSDSEPEAELEAREAKSAKKPQSSSTEPAKPGQKEKRV RPEEKQQA KPVKVE
RTRKRSEGF SMDRKVEKKKEPSVEEKLQKLHSEIKFALKVDSPDVKRCLNLEELGTLQVTSQILQKNTD VVAT
LKKIRRYKANKDVMKAAEVYTRLKSRVLGPKIEAVQKVDKAGMEKEKAEEKLAGEELAGEEAPQEKAEDKPST
DLSAPVNGEATSQKGESAEDEKEHEEGRDSEEGPRCGSSSEDLHESVREGPDLD RPGSDRQERERARGDSEALDEE
S

The Hepatoma Derived Growth Factor-like protein (NOV4b) is expressed in at least the following tissues: lung, blood, lymphocyte, bone marrow, colon, brain, pancreas, pituitary, testis, ovaries, liver, prostate, heart, adrenal gland, spleen, thyroid and uterus.

The amino acid sequence of NOV4b had high homology to other proteins as shown in Table 4F.

Table 4F. BLASTX results for NOV4b

Sequences producing High-scoring Segment Pairs:	Reading Frame	High Score	Smallest Sum Prob P (N)	N
ptnr:SP TREMBL-ACC:O35540 HEPATOMA-DERIVED GROWTH FACTO...+1		2774	6.6e-288	1
ptnr:PIR-ID:JC7168 lens epithelium-derived growth fact...+1		522	4.3e-52	2
ptnr:SP TREMBL-ACC:O75475 LENS EPITHELIUM-DERIVED GROWT...+1		518	1.1e-51	2
ptnr:SP TREMBL-ACC:Q9UER6 TRANSCRIPTIONAL COACTIVATOR P...+1		517	1.4e-51	2
ptnr:TREMBLNEW-ACC:AAF25871 LENS EPITHELIUM-DERIVED GR...+1		503	2.9e-47	1
ptnr:SP TREMBL-ACC:O95368 TRANSCRIPTIONAL COACTIVATOR P...+1		502	3.8e-47	1

NOV4c

A disclosed NOV4c (also referred to as 21143463_A.0.45_EXT) nucleic acid of 2004 nucleotides is shown in Fig. 4G. An open reading frame was identified beginning with an ATG initiation codon at nucleotides 1-3 and ending with a TGA codon at nucleotides 2002-2004.

The start and stop codons are in bold letters in Fig. 4G.

Table 4G. NOV4c Nucleotide Sequence (SEQ ID NO:17).

ATGCCACACGCCCTTCAAGCCCGGGGACTTGGTGTTCGCTAAGATGAAGGGCTACCCTCACTGGCCTGCCAG
GGTGGACGACATCGCGGATGGCGCCGTGAAGCCCCACCCAACAAGTACCCCATCTTTTTCTTTGGCACAC
ACGAAACGGCCCTTCTGGGACCCAAGGACCTGTTCCCTACGACAAATGTAAAGACAAGTACGGGAAGCCC
AACAAGAGGAAAGGCTTCAATGAAGGGCTGTGGGAGATCCAGAACAACCCACGCCAGCTACAGCGCCCC
TCCGCCAGTGAGCTCCTCCGACAGCGAGGCCCCGAGGCCAACCCCGCCGACGGCAGTGACGCTGACGAGG
ACGATGAGGACCGGGGGTTCATGGCCGTACAGCGGTAACCGCCACAGCTGCCAGCGACAGGATGGAGAGC
GACTCAGACTCAGACAAGAGTAGCGACAACAGTGGCCTGAAGAGGAAGACGCCCTGCGCTAAAGGTATCGGT
CTCGAAACGAGCCCCGAAAGGCCCTCCAGCGACCTGGATCAGGCCAGCGTGTCCCATCCGAAGAGGAGAACT
CGGAAAGCTCATCTGAGTCGGAGAAGACGACGACCAGGACTTCACACCTGAGAAGAAAGCAGCGGTCCGG
GCGCCACGGAGGGGCCCTCTGGGGGACGGAAGGCGCCATCAGCCTCCGACTCCGACTCCAA
GGCCGATTCCGACGGGGCCAAGCCTGAGCCGGTGGCCATGGCGCGGTCCGCGTCTCTCTCTCTCTCTCT
CCTCTCTCTCCGACTCCGATGTGTCTGTGAAGAAGCCTCCGAGGGGCGAGGAAGCCAGCGGAGAGCCTCTC
CCGAAGCCGCGAGGGCGGAAACCGAAGCCTGAACGGCCTCCGTCCAGCTCCAGCAGTGACAGTGACAGCGA
CGAGGTGGACCGCATCAGTGAGTGAAGCGGCGGGACGAGGCGCGGAGGCGGAGCTGGAGGCCCGCGCG
GGCGAGAGCAGGAGGAGAGCTGCGGCGCCTGCGGGAGCAGGAGAAGGAGGAGAAGGAGCGGAGCGCGAG
CGGGCCGCTGAGCGGGGACGCGGCGGACGAGCTCAGGGAGGACGATGAGCCCTCAAGAA
GCGGGGACGCAAGGGCCGGGGCCGGGTCCCCCTCTCTCTGACTCCGAGCCCGAGGCCGAGCTGGAGA
GAGAGGCCAAGAAATCAGCGAAGAAGCCGAGTCTCAAGCACAGAGCCCGCCAGGAAACCTGGCCAGAAG
GAGAAGAGAGTGC GGCCCCGAGGAGAAGCAACAAGCCAAGCCCTGAAGGTGGAGCGGACCCGGAAGCGGTC
CGAGGGCTTCTCGATGGACAGGAAGGTAGAGAAGAAGAAAGAGCCCTCCGTGGAGGAGAAGCTGCAGAAGC
TGCACAGTGAGATCAAGTTTGCCCTAAAGGTGACAGCCCGGACGTGAAGAGGTGCCTGAATGCCCTAGAG
GAGCTGGGAACCTGCAGGTGACCTCTCAGATCCTCCAGAAGAACACAGACGTGGTGGCCACCTTGAAGAA
GATTTCGCCGTTACAAAGCGAACAAGGACGTAATGGAGAAGGCAGCAGAAGTCTATACCCGGCTCAAGTCGC
GGGTCTTCGGCCCAAGATCGAGGCGGTGCAGAAAGTGGACAAGGCTGGGATGGAGAAGGAGAAGGCCGAG
GAGAAGCTGGCCGGGGAGGAGCTGGCCGGGGAGGAGGCCCCCCAGGAGAAGGCGGAGGACAAGCCAGCAC
CGATCTCTCAGCCCCAGTGAATGGCGAGGCCACATCACAGAAGGGGGAGAGCGCAGAGGACAAGGAGCACG
AGGAGGGTGGGACTCGGAGGAGGGGCCAAGGTGTGGCTCCTCTGAAGACCTGCACGAGAGCGTACGGGAG
GGTCCCGACCTGGACAGGCCTGGGAGCGACCGGCAGGAGCGCAGAGGGGCACGGGGGGACTCGGAGGCCCT
GGACGAGGAGAGCTGA

In a search of public sequence databases, it was found, for example, that the nucleic acid sequence (NOV4c) has 1570 of 1985 bases (79%) identical to a *Mus musculus* cDNA encoding HET-B which has homology to HDGF mRNA (GENBANK-ID: E14401|acc:E14401)(E = 4.8 e-258).

The NOV4c polypeptide (SEQ ID NO:18) encoded by SEQ ID NO:17 is 667 amino acid residues and is presented using the one-letter amino acid code in Table 4H. The NOV4c protein was analyzed for signal peptide prediction and cellular localization. SignalP, Psort and Hydropathy profile indicate that NOV4c does not have a signal peptide and is likely to be localized in the nucleus. However, the protein predicted here is similar to the "Hepatoma Derived Growth Factor-Like Protein Family", some members of which end up outside the cell and exhibit growth factor activity. Therefore it is likely that NOV4c is available at the appropriate sub-cellular localization and hence accessible for the therapeutic uses described in this application.

Table 4H. NOV4c protein sequence (SEQ ID NO:18)

```

MPHAFKPGDLVFAKMKGYPHWPARVDDIADGAVKPPPNKYPIFFFGTHETAFLGPKDLFFPYDKCKDK
YGKPNKRKGFNEGLWEIQNNPHASYSAPPPVSSSDSEAPEANPADGSDADEDEDRGVMAVTAVTAT
AASDRMESDSDSDKSSDNSGLKRKTPALKVSVSKRARKASSDLDQASVSPSEEENSESSSESEKTS
QDFTPEKKA AVRAPRRGPLGGRKKKKAPSASDSDSKADSDGAKPEPVAMARSASSSSSSSSSSDSDV
SVKKPPRGRKPAEKPLPKPRGRKPKPERPPSSSSSDSDSDEVDRISEWKRRDEARRRELEARRRREQ
EEELRRLREQEKEEKERRRERAAERGGSSGDELREDDEPVKKRGRKGRGRGPPSSSDSEPEAELE
REAKKSAKKPQSSSTEPARKPGQKEKRVRPPEEKQQA KPVKVERTKRSEGFSDMRKVEKKKEPSVEE
KLQKLHSEIKFALKVDSPDVKRCLNALEELGTLQVTSQILQKNTD VVATLKKIRRYKANKDVMKAA
EVYTRLKSRVLGPKIEAVQKVDKAGMEKEKAEK LAGEELAGEEAPQEKAEDKPSTDLSAPVNGEAT
SQKGESAE DKEHEEGRDSEEGPRCGSSEDLHESVREGPD LDRPGSDRQERERARGDSEALDEES

```

The Hepatoma Derived Growth Factor-like protein (NOV4c) maps to chromosome 19 and is expressed in at least the following tissues: adrenal gland, fetal brain, spleen, thyroid and small intestine and additionally from literature sources: testis, ovaries and liver.

- 5 The full amino acid sequence of the NOV4c protein was found to have 552 of 667 amino acid residues (82%) identical to, and 603 of 667 residues (90%) similar to, the 669 amino acid residue Hepatoma Derived Growth Factor-like protein from *Mus musculus* (SPTREMBL-ACC:O35540; E= 6.6 e-288)(Table 4I).

Table 4I. BLASTX results for NOV4c

Sequences producing High-scoring Segment Pairs:	Reading Frame	High Score	Smallest Sum	N
			Prob P(N)	
ptnr:SPTREMBL-ACC:O35540 Hepatoma-Derived GF - Mus	+1	2774	6.6e-288	1

NOV4d

A disclosed NOV4d (also referred to as 117477333_EXT) nucleic acid of 2307 nucleotides is shown in Fig. 4J. An open reading frame was identified beginning with an ATG initiation codon at nucleotides 72-74 and ending with a TGA codon at nucleotides 2085-2087.

- 15 A putative untranslated region upstream from the initiation codon and downstream from the termination codon is underlined in Fig. 4J, and the start and stop codons are in bold letters.

Table 4J. NOV4d Nucleotide Sequence (SEQ ID NO:19).

GCGCGCGCGCGCGCGCGCGCTACCGCGCGCTGCAGCCGCTTTCGCGGCGCTGGGCCTCTCGCCGTGAGC
ATGCCACACGCCTTCAAGCCCGGGGACTTGGTGTTGCTAAGATGAAGGGCTACCTCACTGGCCTGCCAG
 GATCGACGACATCGCGGATGGCGCCGTGAAGCCCCACCCAACAAGTACCCCATCTTTTCTTTGGCACAC
 ACGAAACAGCCTTCTGGGACCCAAGGACCTGTTCCCCTACGACAAATGTAAAGACAAGTACGGGAAGCCC
 AACAAAGAGGAAAGGCTTCAATGAAGGGCTGTGGGAGATCCAGAACAAACCCACGCCAGCTACAGCGCCCC
 TCCGCCAGTGAGCTCCTCCGACAGCGAGGCCCCGAGGCCAACCCGCGACGGCAGTGACGCTGACGAGG
 ACGATGAGGACCGGGGGTCTGAGCCGTACAGCGGTAACCGCCACAGCTGCCAGCGACAGGATGGAGAGC
 GACTCAGACTCAGACAGAGTAGCGACAACAGTGGCCTGAAGAGGAAGACGCCTGCGCTAAAGATGTCGGT
 CTCGAAACGAGCCCCGAAAGGCCTCCAGCGACCTGGATCAGGCCAGCGTGTCCCCATCCGAAGAGGAGAACT
 CGGAAAGCTCATCTGAGTCGGAGAAGACCAGCGACAGGACTTCACACCTGAGAAGAAAGCAGCGGTCCGG
 GCGCCACGGAGGGGCCCTCTGGGGGACGAAAAAAGAAGGCCCATCAGCCTCCGACTCCGACTCCAA
 GGCGATTTCGACGGGGCCAAGCCTGAGCCGGTGGCCATGGCGCGGTGGGCGTCTCTCTCTCTCTCTCT
 CCTCTCTCTCCGACTCCGATGTGTCTGTGAAGAAGCCTCCGAGGGGCGAGGAAGCCAGCGGAGAAGCCTCTC
 CCGAAGCCGCGAGGGCGGAAACCGAAGCCTGAACGGCCTCCGTCCAGCTCCAGCAGTGACAGTGACAGCGA
 CGAGGTGGACCGCATCAGTGAGTGGAAGCGCGGGACGAGGCGCGGAGGCGCGAGCTGGAGGCCCGCGGC
 GCGGAGAGCAGGAGGAGGAGCTGCGGCGCTGCGGGAGCAGGAGAAGGAGGAGAAGGAGCGGAGGCGCGAG
 CGGGCCGACCGCGGGGAGGCTGAGCGGGGACGCGCGGCAGCAGCGGGGACGAGCTCAGGGAGGACGATGA
 GCCCGTCAAGAAGCGGGGACGCAAGGGCCGGGGCCGGGGTCCCCGTCTCTCTGACTCCGAGCCCCGAGG
 CCGAGCTGGAGAGAGAGGCCAAGAAATCAGCGAAGAAGCCGAGTCTCAAGCACAGAGCCCCGCCAGGAAA
 CCTGGCCAGAAGGAGAAGAGAGTGCGGCCCGAGGAGAAGCAACAAGCCAAGCCCGTGAAGGTGGAGCGGAC
 CCGGAAGCGGTCCGAGGGCTTCTCGATGGACAGGAAGGTAGAGAAGAAGAAGAGCCCTCCGTGGAGGAGA
 AGCTGCAGAAGCTGCACAGTGAGATCAAGTTTGCCTTAAAGGTGACAGCCCGGACGTGAAGAGGTGCCTG
 AATGCCCTAGAGGAGCTGGGAACCTGCGAGTGACCTCTCAGATCCTCCAGAAGAACACAGACGTGGTGGC
 CACCTTGAAGAAGATTGCGCGTTACAAAGCGAACAAGGACGTAATGGAGAAGGCAGCAGAAGTCTATACCC
 GGCTCAAGTTCGCGGGTCTCGGCCCAAAGATCGAGGCGGTGCAGAAAGTGAACAAGGCTGGGATGGAGAAG
 GAGAAGGCCGAGGAGAAGCTGGCCGGGGAGGAGCTGGCCGGGGAGGAGGCCCCCAGGAGAAGGCGGAGGA
 CAAGCCAGCACCGATCTCTCAGCCCCAGTGAATGGCGAGGCCACATCACAGAAGGGGGAGAGCGCAGAGG
 ACAAGGAGCACGAGGAGGGTCCGGACTCGGAGGAGGGGCCAAGGTGTGGCTCCTCTGAAGACCTGCACGAC
 AGCGTACGGGAGGGTCCCGACCTGGACAGGCCTGGGAGCGACCGGCAGGAGCGCGAGAGGGCACGGGGGA
 CTCGGAGGCCCTGGACGAGGAGAGCT**GAGCCGCGGGCAGCCAGGCCAGCCCCAGCCCCGCGAGCTCAGGCTGC**
CCCTCTCTCTCCCCGCTCGCAGGAGAGCAGAGCAGAGAAGTGTGGGAACGCTGTGCTGTTTGTATTGT
TCCCTTGGGTTTTTTTTTCTGCTAATTTCTGTGATTTCACCAACATGAAATGACTATAAATGGTTTT
 TTAATGAAAAAAAAAAAAAAAAAGAAAAAAAAAGATT

In a search of public sequence databases, it was found, for example, that the nucleic acid sequence (NOV4d) has 1052 of 1378 bases (76%) identical to a *Mus musculus* Hepatoma Derived Growth Factor-like protein mRNA (GENBANK-ID:D63850)($E = 4.8 \times 10^{-163}$).

The NOV4d polypeptide (SEQ ID NO:20) encoded by SEQ ID NO:19 is 671 amino acid residues and is presented using the one-letter amino acid code in Table 4K. The NOV4d protein was analyzed for signal peptide prediction and cellular localization. SignalP, Psort and Hydropathy profile indicate that NOV4d does not have a signal peptide and is likely to be localized in the nucleus. However, the protein predicted here is similar to the “Hepatoma Derived Growth Factor-Like Protein Family”, some members of which end up outside the cell and exhibit growth factor activity. Therefore it is likely that NOV4d is available at the appropriate sub-cellular localization and hence accessible for the therapeutic uses described in this application.

Table 4K. NOV4d protein sequence (SEQ ID NO:20)

```

MPHAFKPGDLVFAKMGYPHWPARIDDIADGAVKPPPKNKYPIFFFGTHETAFLGPKDLFPYDKCKDKYGKPNKR
KGFNEGLWEIQNNPHASYSAPPPVSSSDSEAPEANPADGSDADEDDDEDRGVMAVTAVTATAASDRMESDSDSDK
SSDNSGLKRKTPALKMSVSKRARKASSDLDQASVSPSEEENSESSSESEKTSQDFTPEKKA AVRAPRRGPLGG
RKKKKAPSASDSDSKADSDGAKPEPVAMARSASSSSSSSSSSDSVSVKKPPRGRKPAEKPLPKPRGRKPKPER
PPSSSSSDSDSDEVDRISEWKRRDEARRRELEARRRREQEELRRLREQEKEEKERRRERADRGEAERGSGGSS
GDELREDDEPVKKRGRKGRGRGPPSSSDSEPEAELEAREAKKSAKKPQSSSTEPARKPGQKEKRVRPPEKQQAQK
VKVERTKRKRSEGFMDRKVEKKKEPSVEEKLQKLHSEIKFALKVDS PDVKRCLNALEELGTLQVTSQILQKNTD
VVATLKKIRRYKANKDVMKAAEVYTRLKSRVLGPKIEAVQKVNKAGMEKEKAEKLAGEEELAGEEAPQEKAEED
KPSTDLSAPVNGEATSQKGESAEDKEHEEGRDSEEGPRCGSSEDLHDSVREGPDLD RFGSDRQERERARGDSEA
LDEES

```

The Hepatoma Derived Growth Factor-like protein (NOV4d) maps to chromosome 19 and is expressed in at least the following tissues: brain, heart, lung, lung carcinoids, exocrine pancreas, breast, teratocarcinoma, ovarian tumor, prostate, colon, colon carcinoma, esophagus, foreskin, germ cells, uterus, genitourinary tract, thyroid, blood, spleen, tonsil, hematopoietic and lymphatic systems and bone marrow.

The full amino acid sequence of the NOV4d protein was found to have 563 of 671 amino acid residues (82%) identical to, and 603 of 671 residues (89%) similar to, the 669 amino acid residue Hepatoma Derived Growth Factor-like protein from *Mus musculus* (SPTREMBL-ACC:O35540; E= 2.7 e-288).

The amino acid sequence of NOV4d had high homology to other proteins as shown in Table 4L.

Table 4L. BLASTX results for NOV4d

Sequences producing High-scoring Segment Pairs:	Reading Frame	High Score	Smallest Sum Prob P(N)	N
ptnr:SPTREMBL-ACC:O35540 HEPATOMA-DERIVED GROWTH FACTO..+3		2777	2.7e-288	1
ptnr:PIR-ID:JC7168 lens epithelium-derived growth fact..+3		522	5.8e-52	2
ptnr:SPTREMBL-ACC:O75475 LENS EPITHELIUM-DERIVED GROWT..+3		518	1.8e-51	2

NOV4a, 4b, 4c and 4d are related to each other as shown in the alignment listed in Table 4M.

[illegible]

10 20 30 40 50 60

MPNFAFKPGDLVFAFKMGYPHWPARIDDIADGAVKPPPNKYPIFFFGTHETAFLGPKDLFF
MPHAFKPGDLVFAFKMGYPHWPARIDDIADGAVKPPPNKYPIFFFGTHETAFLGPKDLFF
MPHAFKPGDLVFAFKMGYPHWPARIDDIADGAVKPPPNKYPIFFFGTHETAFLGPKDLFF
MPHAFKPGDLVFAFKMGYPHWPARIDDIADGAVKPPPNKYPIFFFGTHETAFLGPKDLFF

70 80 90 100 110 120

YDKCKDKYKGPKNRKGNEGLWEIQNNPHASYSAPPPVSSSDSEAPEANPADGSDADEDD
YDKCKDKYKGPKNRKGNEGLWEIQNNPHASYSAPPPVSSSDSEAPEANPADGSDADEDD
YDKCKDKYKGPKNRKGNEGLWEIQNNPHASYSAPPPVSSSDSEAPEADLGGCSDYDKDK
YDKCKDKYKGPKNRKGNEGLWEIQNNPHASYSAPPPVSSSDSEAPEADLGGCSDYDKDK
YDKCKDKYKGPKNRKGNEGLWEIQNNPHASYSAPLPVSSSDSEAPEADLGGCSDADKEK

130 140 150 160 170 180

EDRGVMAVTAVTTATAASDRMESDSDSKSSDNGSLKRKTPALKVSVSKRARKASSDLDQA
EDRGVMAVTAVTTATAASDRMESDSDSKSSDNGSLKRKTPALKVSVSKRARKASSDLDQA
ESRRVMTVTAVTTATATSDRMESDSDSDSKSSDNGSLKRKTPVLKVSVSKRARKASSDLDQA
ESRRVMTVTAVTTATATSDRMESDSDSDSKSSDNGSLKRKTPVLKVSVSKRARKASSDLDQA
EARRVMTVTAVTTATATSGRTESDSDSDSKSSDNGSLKRKTPVLKVSVSKRARKASSDLDQA

190 200 210 220 230 240

SVSPSEEEENSESSSESEKTSDDQDFTPEKKA AVRAPRRGPLGGRKK-----KKAPSA
SVSPSEEEENSESSSESEKTSDDQDFTPEKKA AVRAPRRGPLGGRKK-----KKAPSA
SVSPSEED--SESPSESEKTSDDQDFTPEKKTAA RPPRRGPLGGRKKKHPTGYACPGVPSA
SVSPSEED--SESPSESEKTSDDQDFTPEKKTAA RPPRRGPLGGRKK-----KKVPSA
SVSPSEED--SESPSESEKTSDDQDFTPEKKTAA RPPRRGPLGGRKK-----KKVPSA

250 260 270 280 290 300

SDSDSKADSDGAKPEPVAMAR--SASSSSSSSSSSSDSDSVSVKKPPRGRKPAEKPLPKPR
SDSDSKADSDGAKPEPVAMAR--SASSSSSSSSSSSDSDSVSVKKPPRGRKPAEKPLPKPR
SDSDSKADSDGAKPEPVTAQPSFSSSSSSSSSSSSSDSDSVSVKKPPRGRKPAEKPPKPR
SDSDSKADSDGAKPEPVTAQPSFSSSSSSSSSSSSSDSDSVSVKKPPRGRKPAEKPPKPR
SDSDSRADSDGAKPEPVTAQPSFSSSSSSSSSSSSSDSDSVSVKKPPRGRKPAEKPPKPR

310 320 330 340 350 360

GRKPKPERPPSSSSSDSDSD--EVDRISEWKRRDEARRRELEARRRREQEELRLRLREQE
GRKPKPERPPSSSSSDSDSD--EVDRISEWKRRDEARRRELEARRRREQEELRLRLREQE
GRKPKPERPPSTSSSDSDSDSGEVDRISEWKRRDEARRRELEARRRREQEELRLRLREQE
GRKPKPERPPSTSSSDSDSDSGEVDRISEWKRRDEARRRELEARRRREQEELRLRLREQE
GRKPKPERPPSTSSSDSDSDSGEVDRISEWKRRDEARRRELEARRRREQEELRLRLREQE

370 380 390 400 410 420

KEEKERRRERADRGAEARGSGGSSGDELREDEFPVKRGRKGRGRGPPSSSDSEPEAELE
KEEKERRRERADRGAEARGSGGSSGDELREDEFPVKRGRKGRGRGPPSSSDSEPEAELE
REEKERRKERAE-----GGSSGEELE-DEFPVKRGRKGRGRGTPSSSDSEPEGELG
REEKERRKERAE-----GGSSGEELE-DEFPVKRGRKGRGRGTPSSSDSEPEGELG
REEKERRKERAE-----GGSSGEELE-DEFPVKRGRKGRGRGTPSSSDSEPEGELG

430 440 450 460 470 480

REAKKSAKKPQSSSTEPARKPGQKEKRVPEEKQOARPVKVVERTRKRSEGSMDRKEKK
REAKKSAKKPQSSSTEPARKPGQKEKRVPEEKQOARPVKVVERTRKRSEGSMDRKEKK
KEGKKLAKKSOLPGSESARKPGQKEKGRPDEKPRARPVKVVERTRKRSEGLSLERNGEKK
KEGKKLAKKSOLPGSESARKPGQKEKGRPDEKPRARPVKVVERTRKRSEGLSLERNGEKK
KEGKKLAKKSOLPGSESARKPGQKEKGRPDEKPRARPVKVVERTRKRSEGLSLDRNGEKK

490 500 510 520 530 540

KEPSVEEKLQKLHSEIKFALKVDSPDVKRCLNALEELGLTQVTSQILQKNTDVVATLKKI
KEPSVEEKLQKLHSEIKFALKVDSPDVKRCLNALEELGLTQVTSQILQKNTDVVATLKKI
KEPSVEERLQKLHSEIKFALKVDNPDVVRCLSALEELGLTQVTSQILQKNTDVVATLKKI
KEPSVEERLQKLHSEIKFALKVDNPDVVRCLSALEELGLTQVTSQILQKNTDVVATLKKI
KEPSVEERLQKLHSEIKFALKVDNPDVVRCLSALEELGLTQVTSQILQKNTDVVATLKKI

550 560 570 580 590 600

5	NOV4A gi 12653923 gi 13277669 gi 6680201 gi 13957749	<pre> RRYKANKDVMKAAEVYTRLKSRVLGPKIEAVQVKNKAGMEKEKAEKLAGELAGEELA RRYKANKDVMKAAEVYTRLKSRVLGPKIEAVQVKNKAGMEKE-----KAEKLAGELAGEELA RRYKANKDVMKAAEVYTRLKSRVLGPKIEAVQVKNKAGMEKE-----RADNEKLEEQP RRYKANKDVMKAAEVYTRLKSRVLGPKIEAVQVKNKAGMEKE-----RADNEKLEEQP RRYKANKDVMKAAEVYTRLKSRVLGPKIEAVQVKNKAGMEKE-----RADGEKVLEEQP </pre>
10	NOV4A gi 12653923 gi 13277669 gi 6680201 gi 13957749	<pre> 610 620 630 640 650 660 GEEAPQEKAEADKPSTDLAPVNGEATSQKGESAEDEKEHEEGRDSEEGPRCGSSEDLHESV GEEAPQEKAEADKPSTDLAPVNGEATSQKGESAEDEKEHEEGRDSEEGPRCGSSEDLHDVR GEEAPQEKAEADKPSTDLAPVNGEATSQKGENMEDRAQEDGQDSEEGPRCGSSEDLHDSV GEEAPQEKAEADKPSTDLAPVNGEATSQKGENMEDRAQEDGQDSEEGPRCGSSEDLHDSV GEEAPQEKAEADKPSTDLAPVNGEATSQKGENMEDRAQEDGQDSEEGPRCGSSEDLHDSV </pre>
15	NOV4A	<pre> 670 680 690 REGPDLDPRGSDRQERERARGDSEALD---EES REGPDLDPRGSDRQERERARGDSEALD---EES </pre>
20	NOV4A gi 12653923 gi 13277669 gi 6680201 gi 13957749	<pre> RDNSDPAKPGNERODHERTRLASESANDDNEDS RDNSDPAKPGNERODHERTRLASESANDDNEDS RDNSDPAKPGNERODHERTRLASESANDDNEDS RDNSDPAKPGNERODHERTRLASESANDDNEDS RDNSDPAKPGNERODHERTRLASESANDDNEDS </pre>

The homologies shown above are shared by NOV4b, 4c and 4d insofar as they are themselves homologous to NOV4a as shown in Table 4M.

Table 4P lists the domain description from DOMAIN analysis results against NOV4a. This indicates that the NOV4a sequence has properties similar to those of other proteins known to contain this domain.

Table 4P. Domain Analysis of NOV4a

gnl|Pfam|pfam00855, PWWP, PWWP domain. (SEQ ID NO:55)
CD-Length = 74 residues, 98.6% aligned
Score = 76.6 bits (187), Expect = 4e-15

30	NOV4A	<pre> 10 20 30 40 50 60 AFKPGDLVFPKIKGYPOWPSRIDDI-ADGAVK-----PPPN </pre>
35	Pfam_pfam00855	<pre> DFKPGDLVWAKMKGEPPWWPARIISPKETPTSV-----AKDN </pre>
40	NOV4A	<pre> 70 80 90 100 KYPPIFFFGTHET-ARLCPKDLFPY--DKCKDKYKPNKRKG </pre>
	Pfam_pfam00855	<pre> RYKVLFFGDKHT-AWISPSKLLKPL--DVDLEKEHKDRKRKG </pre>

Other BLAST results include sequences from the Patp database, which is a proprietary database that contains sequences published in patents and patent publications. Patp results include those listed in Table 4Q

Table 4Q. Patp alignments of NOV4

Sequences producing High-scoring Segment Pairs:			Smallest	
	Reading	High	Sum	
	Frame	Score	Prob.	P (N)
Patp:AA99426 Human PRO1604 (UNQ785), <i>Homo sapiens</i> , 671aa	+1	3379	0.0	
Patp:AAB66175 unidentified protein, 671 aa	+1	3379	0.0	

For example, a BLAST against patp:AA99426, a 671 amino acid polypeptide (WO00/012708) from *Homo sapiens*, produced good identity, E = 0.0. Additionally, a BLAST against patp:AAB66175, a 671 unidentified protein (WO00/78961), also produced good identity, E=0.0.

Hepatoma-Derived Growth Factor (HDGF) is a basis Fibroblast Growth Factor-like growth factor secreted by human hepatomas that acts as an endothelial cell mitogen (Klagsbrun et al., 1986). It is expressed in proliferating smooth muscle cells and may be involved in vascular development and atherosclerosis (Everett et al., 2000). HDGF has also been implicated in renal development (Oliver et al., 1998).

Many groups have attempted to elucidate the specific function(s) of HDGF; as its role in vascular growth is currently unknown. Everett et al. (2000) demonstrated that HDGF mRNA is expressed in smooth muscle cells (SMCs), most prominently in proliferating SMCs. Exogenous HDGF and endogenous overexpression of HDGF stimulated a significant increase in SMC number and DNA synthesis. Moreover, it was shown that HDGF colocalizes with the proliferating cell nuclear antigen (PCNA) in SMCs in human atherosclerotic carotid arteries, suggesting that HDGF helps regulate SMC growth during development and in response to vascular injury. Cilley et al. (2000) while studying lung development identified HDGF as a differentially expressed gene enhanced by tracheal ligation using an in vitro murine fetal lung model with airway ligation. The authors concluded that genes enhanced by airway pressure or tracheal ligation are mitogenic for fibroblasts, correlate with cell proliferation, regulate cell proliferation and differentiation, and may play a role in growth in distal lung and type II cell differentiation. Oliver et al., 1998 while studying the potential secretion of endothelial mitogens by metanephrogenic mesenchymal cells using a endothelial mitogenic assay and sequential chromatography isolated HDGF. The authors found that HDGF was widely distributed in the renal anlage at early stages of development but soon concentrated at sites of active morphogenesis and, except for some renal tubules, disappeared from the adult kidney.

HDGF was most abundant at sites of nephron morphogenesis and in ureteric bud cells while in the adult kidney transcripts disappeared except for a small population of distal tubules. Thus, the authors concluded that HDGF is an endothelial mitogen that is present in embryonic kidney, and its expression is synchronous with nephrogenesis

5 Along with HDGF, there is a family of proteins with significant homology to HDGF in the amino terminal region (hath region) which are termed HDGF-related proteins (HRPs) (Izumoto et al., 1997)(Ikegame et al., 1999). There are several family members with varied tissue expression. HRP-1 is expressed only in the developing germ cells of the testis and may be involved in spermatogenesis. These findings suggest that the testis-specific HRP-1 gene
10 may play an important role in the phase around meiotic cell division (Kuroda et al., 1999). HRP-2, like HDGF, is expressed predominantly in the testis and skeletal muscle, with intermediate levels in heart, brain, lung, liver and kidney and minimally in the spleen. HRP-1 is a highly acidic protein (26% acidic) and also has a putative NLS. HRP-2 protein carries a mixed charge cluster (Izumoto et al., 1997). HRP-3 cDNA contained 203 amino acids without a signal
15 peptide for secretion. HRP-3 has a putative bipartite nuclear localizing signal (NLS) sequence and as a result is known to translocate to the nucleus. The HRP-3 gene was mapped to chromosome 15, region q25 by FISH analysis. Further, HRP-3 is expressed predominantly in the testis and brain, to an intermediate extent in the heart, and with lower levels in the ovaries, kidneys, spleen, and liver in humans (Ikegame et al., 1999).

20 The expression pattern, map location and protein similarity information for the invention(s) suggest that these NOV4 proteins may function as members of the HDGF family. Therefore, the nucleic acids and proteins of the invention are useful in potential therapeutic applications implicated, for example but not limited to, in various pathologies /disorders as described below and/or other pathologies/disorders. Potential therapeutic uses for the
25 invention(s) are, for example but not limited to, the following: Protein therapeutic, small molecule drug target, antibody target (therapeutic, diagnostic, drug targeting/cytotoxic antibody), diagnostic and/or prognostic marker, gene therapy (gene delivery/gene ablation), research tools, and tissue regeneration *in vitro* and *in vivo* (regeneration for all these tissues and cell types composing these tissues and cell types derived from these tissues).

30 The nucleic acids and proteins of the invention are useful in potential therapeutic applications implicated in various diseases and disorders described below and/or other

pathologies and disorders. For example, but not limited to, a cDNA encoding the HDGF-like protein may be useful in gene therapy, and the HDGF-like protein may be useful when administered to a subject in need thereof. By way of nonlimiting example, the compositions of the present invention will have efficacy for treatment of patients suffering from

5 Adrenoleukodystrophy, Congenital Adrenal Hyperplasia, Hyperthyroidism, Inflammatory bowel disease, Diverticular disease, Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura, Immunodeficiencies, Graft versus host, Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, 10 Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection, Fertility, Cirrhosis, Transplantation. The novel nucleic acid encoding the HDGF-like protein, and the HDGF-like protein of the invention, or fragments thereof, may further be useful in diagnostic applications, wherein the presence or amount of the nucleic acid or the protein are to be assessed. These materials are further useful in the generation of 15 antibodies that bind immunospecifically to the novel substances of the invention for use in therapeutic or diagnostic methods.

The novel nucleic acids encoding HDGF-like proteins, and the HDGF-like proteins of the invention, or fragments thereof, may further be useful in diagnostic applications, wherein the presence or amount of the nucleic acid or the protein are to be assessed. These materials are 20 further useful in the generation of antibodies that bind immunospecifically to the novel substances of the invention for use in therapeutic or diagnostic methods and other diseases, disorders and conditions of the like. These materials are further useful in the generation of antibodies that bind immunospecifically to the novel substances of the invention for use in therapeutic or diagnostic methods. These antibodies may be generated according to methods 25 known in the art, using prediction from hydrophobicity charts, as described in the "Anti-NOVX Antibodies" section below.

For example, the disclosed NOV4 proteins have multiple hydrophilic regions, each of which can be used as an immunogen. In one embodiment, a contemplated NOV4 epitope is from about amino acids 10 to 50. In another embodiment, a NOV4 epitope is from about amino 30 acids 55 to 125. In additional embodiments, NOV4 epitopes are from about amino acids 130 to 500 and from about amino acids 520 to 680. These novel proteins can be used in assay systems

for functional analysis of various human disorders, which will help in understanding of pathology of the disease and development of new drug targets for various disorders.

NOV5

NOV5a

5 This invention describes the following novel Cortexin-like proteins and nucleic acids encoding them: 21647246_EXT. These sequences were initially identified by searching CuraGen's Human SeqCalling database for DNA sequences, which translate into proteins with similarity to Cortexin-Like Proteins. SeqCalling assembly 21647246 was identified as having suitable similarity. SeqCalling assembly 21647246 was analyzed further to identify any open
10 reading frames encoding novel full length proteins as well as novel splice forms of these genes. The SeqCalling assembly was extended using one or more sequences taken from additional SeqCalling assemblies, publicly available EST sequences and public genomic sequences. Public ESTs and additional CuraGen SeqCalling assemblies were identified by the CuraTools™ program SeqExtend. Such fragments were included in the DNA sequence extension for
15 SeqCalling assembly 21647246 only when the extent of identity in the putative overlap region was high. The extent of identity may be, for example, about 90% or higher, preferably about 95% or higher, and even more preferably close to or equal to 100%. These inclusions, if used, are described below.

The following genomic clones were identified as having regions with 100% identity to
20 the SeqCalling assembly 21647246. They were selected for analysis because this identity indicates that these clones identify the genomic locus for SeqCalling assembly 21647246.

Genomic clone acc:AC010336 Homo sapiens chromosome 19 clone CITB-E1_3193O13, WORKING DRAFT SEQUENCE, 64 unordered pieces - *Homo sapiens* was analyzed by Genscan and Grail to identify exons and putative coding sequences. This clone
25 was also analyzed by TblastN, BlastX and other programs to identify genomic regions translating to proteins with similarity to the original protein or protein family of interest.

The results of these analyses were integrated and manually corrected for apparent inconsistencies that may have arisen, for example, from miscalled bases in the original fragments used. The sequences obtained encode the full-length proteins disclosed herein. When
30 necessary, the process to identify and analyze cDNAs, ESTs and genomic clones was reiterated

to derive the full-length sequence. This invention describes the resulting full-length DNA sequence and the full-length protein sequence, which they encode.

The disclosed NOV5a nucleic acid of 249 nucleotides (also referred to as CuraGen Acc. No. 21647246_EXT) encoding a novel Cortixin-like protein is shown in Table 5A. An ORF
5 begins with an ATG initiation codon at nucleotides 1-3 and ends with a TGA codon at nucleotides 247-249. The start and stop codons are in bold letters in Table 5A.

Table 5A. NOV5a Nucleotide Sequence (SEQ ID NO:21)

ATG AGCGCGACGTGGACGCTGTCGCCGGAGCCCCTGCCGCCGTCGACGGGGCCCCCGGTGGGCGCGGGCC TGGACGCGGAGCAGCGCACGGGTGTTTCGCCTTCGTGCTCTGCCTGCTCGTGGTGCTGGTGCTGTTGATGGT GCGCTGCGTGCGCATCCTGCTCGACCCCTACAGCCGCATGCCCGCCTCGTCCTGGACCGACCACAAGGAG GCGCTCGAGCGCGGGCAGTTCGACTACGCGTTGGTG TGA

The NOV5a protein encoded by SEQ ID NO:21 has 82 amino acid residues and is
10 presented using the one-letter code in Table 5B. The Psort profile for NOV5a predicts that this sequence has a signal peptide and is likely to be localized at the plasma membrane with a certainty of 0.700, it may also localize to the microbody (peroxisome) (certainty of 0.2462); endoplasmic reticulum (membrane) (certainty of 0.200); and mitochondrial inner membrane (certainty of 0.1000). The most likely cleavage site for a peptide is between amino acids 49 and
15 50, *i.e.*, at the slash in the amino acid sequence VRC-VR based on the SignalP result.

The disclosed Cortixin-like protein maps to chromosome 19. Moreover, the disclosed protein is expressed in atleast the following tissues: cortex (brain), hippocampus (brain), and nervous system.

Table 5B. Encoded NOV5a protein sequence (SEQ ID NO:22)

MSATWTLSPPEPLPPSTGPPVGAGLDAEQRTVFAFVLCLLVVLVLLMVRCVRILLDPYSRMPASSWTDHKEAL ERGQFDYALV

NOV5b

In the present invention, the target sequence identified previously, Accession Number 21647246_EXT (NOV5a), was subjected to the exon linking process to confirm the sequence. PCR primers were designed by starting at the most upstream sequence available, for the forward primer, and at the most downstream sequence available for the reverse primer. In each
25 case, the sequence was examined, walking inward from the respective termini toward the coding sequence, until a suitable sequence that is either unique or highly selective was encountered, or, in the case of the reverse primer, until the stop codon was reached. Such

primers were designed based on in silico predictions for the full length cDNA, part (one or more exons) of the DNA or protein sequence of the target sequence, or by translated homology of the predicted exons to closely related human sequences sequences from other species. These primers were then employed in PCR amplification based on the following pool of human

5 cDNAs: adrenal gland, bone marrow, brain - amygdala, brain - cerebellum, brain - hippocampus, brain - substantia nigra, brain - thalamus, brain -whole, fetal brain, fetal kidney, fetal liver, fetal lung, heart, kidney, lymphoma - Raji, mammary gland, pancreas, pituitary gland, placenta, prostate, salivary gland, skeletal muscle, small intestine, spinal cord, spleen, stomach, testis, thyroid, trachea, uterus. Usually the resulting amplicons were gel purified,
10 cloned and sequenced to high redundancy. The resulting sequences from all clones were assembled with themselves, with other fragments in CuraGen Corporation's database and with public ESTs. Fragments and ESTs were included as components for an assembly when the extent of their identity with another component of the assembly was at least 95% over 50 bp. In addition, sequence traces were evaluated manually and edited for corrections if appropriate.
15 These procedures provide the sequence reported below, which is designated Accession Number 21647246_da1 (NOV5b) which is 100% homologous to the previously identified sequence (Accession Number 21647246_EXT).

The NOV5b sequence of the invention was derived by laboratory cloning of cDNA fragments covering the full length and/or part of the DNA sequence of the invention, and/or by
20 *in silico* prediction of the full length and/or part of the DNA sequence of the invention from public human sequence databases.

The laboratory cloning was performed using one or more of the methods summarized below:

Exon Linking: The cDNA coding for the sequence was cloned by polymerase chain
25 reaction (PCR) using the following primers: ATGAGCGCGACGTGGACG (SEQ ID NO:101) and TCACACCAACGCGTAGTCGAACT (SEQ ID NO:102 on the following pools of human cDNAs: Pool 1 - Adrenal gland, bone marrow, brain - amygdala, brain - cerebellum, brain - hippocampus, brain - substantia nigra, brain - thalamus, brain -whole, fetal brain, fetal kidney, fetal liver, fetal lung, heart, kidney, lymphoma - Raji, mammary gland, pancreas, pituitary
30 gland, placenta, prostate, salivary gland, skeletal muscle, small intestine, spinal cord, spleen, stomach, testis, thyroid, trachea, uterus.

Primers were designed based on *in silico* predictions for the full length or part (one or more exons) of the DNA/protein sequence of the invention or by translated homology of the predicted exons to closely related human sequences or to sequences from other species. Usually multiple clones were sequenced to derive the sequence which was then assembled similar to the SeqCalling process. In addition, sequence traces were evaluated manually and edited for corrections if appropriate.

Physical clone: The PCR product derived by exon linking was cloned into the pCR2.1 vector from Invitrogen. The bacterial clone 120906::21647246.698361.M22 has an insert covering the entire open reading frame cloned into the pCR2.1 vector from Invitrogen.

Variant sequences are also included in this application. A variant sequence can include a single nucleotide polymorphism (SNP). A SNP can, in some instances, be referred to as a "cSNP" to denote that the nucleotide sequence containing the SNP originates as a cDNA. A SNP can arise in several ways. For example, a SNP may be due to a substitution of one nucleotide for another at the polymorphic site. Such a substitution can be either a transition or a transversion. A SNP can also arise from a deletion of a nucleotide or an insertion of a nucleotide, relative to a reference allele. In this case, the polymorphic site is a site at which one allele bears a gap with respect to a particular nucleotide in another allele. SNPs occurring within genes may result in an alteration of the amino acid encoded by the gene at the position of the SNP. Intragenic SNPs may also be silent, however, in the case that a codon including a SNP encodes the same amino acid as a result of the redundancy of the genetic code. SNPs occurring outside the region of a gene, or in an intron within a gene, do not result in changes in any amino acid sequence of a protein but may result in altered regulation of the expression pattern for example, alteration in temporal expression, physiological response regulation, cell type expression regulation, intensity of expression, stability of transcribed message.

The DNA sequence and protein sequence for a novel Cortexin-like gene or one of its splice forms was obtained solely by exon linking and is reported here as NOV5b.

In the following positions, one or more consensus positions (Cons. Pos.) of the nucleotide sequence have been identified as SNPs. "Depth" rerepresents the number of clones covering the region of the SNP. The Putative Allele Frequency (Putative Allele Freq.) is the fraction of all the clones containing the SNP. A dash ("-"), when shown, means that a base is not present. The sign ">" means "is changed to".

Cons.Pos.: 24 Depth: 48 Change: G > A
Cons.Pos.: 39 Depth: 48 Change: A > C

	Cons.Pos.: 40	Depth: 48	Change: G > A
	Cons.Pos.: 63	Depth: 57	Change: C > T
	Cons.Pos.: 68	Depth: 57	Change: A > C
5	Cons.Pos.: 72	Depth: 57	Change: A > G
	Cons.Pos.: 110	Depth: 57	Change: A > G
	Cons.Pos.: 146	Depth: 56	Change: C > G
	Cons.Pos.: 170	Depth: 56	Change: T > C
	Cons.Pos.: 177	Depth: 56	Change: G > C
10	Cons.Pos.: 297	Depth: 54	Change: T > C
	Cons.Pos.: 309	Depth: 54	Change: C > T
	Cons.Pos.: 439	Depth: 66	Change: T > C
	Cons.Pos.: 445	Depth: 66	Change: A > G
	Cons.Pos.: 479	Depth: 64	Change: G > A
15	Cons.Pos.: 488	Depth: 61	Change: T > C
	Cons.Pos.: 492	Depth: 60	Change: T > C
	Cons.Pos.: 511	Depth: 61	Change: C > T
	Cons.Pos.: 524	Depth: 63	Change: C > T
	Cons.Pos.: 539	Depth: 62	Change: C > T
20	Cons.Pos.: 626	Depth: 38	Change: C > T
	Cons.Pos.: 708	Depth: 43	Change: T > G
	Cons.Pos.: 720	Depth: 44	Change: T > C
	Cons.Pos.: 753	Depth: 44	Change: C > G
	Cons.Pos.: 852	Depth: 44	Change: G > T
25	Cons.Pos.: 872	Depth: 44	Change: A > G
	Cons.Pos.: 878	Depth: 44	Change: T > C
	Cons.Pos.: 904	Depth: 44	Change: C > T
	Cons.Pos.: 956	Depth: 46	Change: C > T
	Cons.Pos.: 980	Depth: 46	Change: A > G

30 As shown in Tables 5C and 5D, the disclosed NOV5a and NOV5b nucleic acid sequences and amino acid sequences are 100% identical. As used herein, any reference to NOV5 encompasses both NOV5a and NOV5b.

Table 5C. Sequence Alignment of NOV5a and NOV5b Nucleic Acid Sequences	
	10 20 30 40 50 60
NOV5a
NOV5b	ATGAGCGCGACGTGGACGCTGTCGCCGGAGCCCTGCCGCCGTCGACGGGGCCCCCGGTG
	70 80 90 100 110 120
NOV5a
NOV5b	GGCGCGGGCCTGGACGCGGAGCAGCGCACGGTGTTCGCCTTCGTGCTCTGCCTGCTCGTG
	130 140 150 160 170 180
NOV5a
NOV5b	GTGCTGGTGTGTTGATGGTGGCTGCGCTGCGCATCCTGCTCGACCCCTACAGCCGCATG
	190 200 210 220 230 240
NOV5a
NOV5b	CCCGCCTCGTCCTGGACCGACCACAAGGAGGCGCTCGAGCGCGGGCAGTTCGACTACGCG

NOV5a	TTGGTGTGA (SEQ ID NO:21)
NOV5b	TTGGTGTGA (SEQ ID NO:21)

Table 5D. Sequence Alignment of NOV5a and NOV5b Amino Acid Sequences	
	10 20 30 40 50 60
NOV5a
NOV5b	MSATWTLSPPEPLPPSTGPPVGAGLDAEQRTVFAFVLCLLVVLVLLMVRCVRILLDPYSRM
	70 80
NOV5a
NOV5b	PASSWTDHKEALERGQFDYALV (SEQ ID NO:22)
	PASSWTDHKEALERGQFDYALV (SEQ ID NO:22)

The disclosed nucleic acid sequence for NOV5 has 229 of 249 bases (91 %) identical and 229 of 249 (91%) residues positives to a *Rattus norvegicus* neuron-specific cortixin mRNA (acc:L15011) (E=4.2e-42).

Moreover, the full NOV5 amino acid sequence of the protein of the invention was found to have 46 of 82 amino acid residues (56 %) identical to, and 46 of 82 residues (56%) positive

with, the 82 amino acid residue rat cortexin. (gi|729225|sp|P41237|CTXN_RAT CORTEXIN; gi|543376|pir|JH0814 (cortexin - rat)) (E=2e-15).

The disclosed NOV5 protein has good identity with a cortexin-like protein. The identity information used for ClustalW analysis is presented in Table 5E.

5

Table 5E. BLAST results for NOV5					
Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
gi 729225 sp P41237 CTXN_RAT CORTEXIN; gi 543376 pir JH0814 cortexin	cortexin <i>Rattus norvegicus</i>	82	46/82 (56%)	46/82 (56%)	2e-15

This information is presented graphically in the Clustal W sequence alignment given in Table 5F (with NOV5 being shown on line 1) comparing NOV5 with a related protein sequence.

10

Table 5F Clustal W Sequence Alignment:

1) NOV5 (SEQ ID NO:22)

2) gi|729225|sp|P41237|CTXN_RAT CORTEXIN (SEQ ID NO:56)

	10	20	30	40	50	60
CURA326 21647246_EXT PRT	MSA	NTLSPEPLPPSTGPPVGAGL	FEORTVFAFVLCLLVVLVLLMVRCVRTLLDPYSRF			
gi 729225	MSA	NTLSPEPLPPSTGPPVGAGL	FEORTVFAFVLCLLVVLVLLMVRCVRTLLDPYSRF			
	70	80				
CURA326 21647246_EXT PRT	PASSWTDHKEALERGQFDYALV					
gi 729225	PASSWTDHKEALERGQFDYALV					

15

The NOV5 proteins predicted here are similar to the “Cortexin-Like Protein Family”, some members of which end up localized at the cell surface where they exhibit activity. Therefore, it is likely that the novel Cortexin-like proteins are available at the appropriate sub-cellular localization and hence accessible for the therapeutic uses described herein.

20

Nucleotide sequence analysis of a cDNA clone of a rat cortex-enriched mRNA identifies a novel integral membrane protein of 82 amino acids. The encoded protein is named cortexin to reflect its enriched expression in cortex. The amino acid sequence of rat cortexin and its mouse homologue are nearly identical (98% similarity), and both contain a conserved

single membrane-spanning region in the middle of each sequence. Northern blot analysis shows that cortexin mRNA is brain-specific, cortex-enriched, and present at significant levels in fetal brain, with peak expression in postnatal rodent brain. *In situ* hybridization studies detect cortexin mRNA primarily in neurons of rodent cerebral cortex, but not in cells of the hindbrain or white matter regions. The function of cortexin may be particularly important to neurons of both the developing and adult cerebral cortex. See *J. Neurochem* 61(2):756-59 (1993).

A clinical trial of cortexin, a new peptide bioregulator of cerebral functions, in combined therapy of dyscirculatory encephalopathy (DE) stage I-II was made in 76 patients. They were divided into two groups: a control group of 31 patients on standard therapy and the study group of 45 patients on standard therapy with adjuvant cortexin delivered via nasal electrophoresis (NE). The effect was estimated by clinical symptoms, psychophysiological tests, computed EEG, quantitative parameters of rehabilitation. Cortexin NE produced a positive effect on psychoemotional state, neurological status, intellectual-mnemonic and CNS functions. Adjuvant cortexin aroused efficiency of rehabilitation in DE stage I and II by 22.7%. The response of intellectual-mnemonic and CNS functions was the highest. Cortexin improves attention, perception, memory, thinking, cortical neurodynamic processes. It is well tolerated and has no side effects. Cortexin is recommended as a drug of choice in combined treatment of patients with DE stage I-II. See *Klin Med. (Mosk)* 77(4):42-45 (1999).

The effect of cortexin and epithalamin on the cell growth rate was investigated in the organotypic tissue culture of dorsal root ganglia (DRG), and of cortex and subcortical structures of 10-11-day old chick embryos. Cortexin in concentrations of 20 and 100 ng/ml is active, inducing a more intensive neurite outgrowth in DRG, compared to the control. Epithalamin was active in concentrations 20 and 200 ng/ml. Cortexin (100 ng/ml) was active in the cortex tissue culture, but inhibited the neurite growth in the subcortical structures culture. The stimulation of this culture to development was evident after using 200 ng/ml epithalamin. The neurite stimulating effect of cortexin and epithalamin is presumably associated with neurotrophic factors. See *Tsitologiya* 39(7):571-76 (1997).

The expression pattern, map location and protein similarity information for the invention suggest that this Cortexin-like protein may function as a member of the Cortexin-like protein family. Therefore, the nucleic acids and proteins of the invention are useful in potential therapeutic applications implicated, for example but not limited to, in various pathologies /disorders as described below and/or other pathologies/disorders. Potential therapeutic uses for

the invention(s) are, for example but not limited to, the following: (i) Protein therapeutic, (ii) small molecule drug target, (iii) antibody target (therapeutic, diagnostic, drug targeting/cytotoxic antibody), (iv) diagnostic and/or prognostic marker, (v) gene therapy (gene delivery/gene ablation), (vi) research tools, and (vii) tissue regeneration *in vitro* and *in vivo* (regeneration for all these tissues and cell types composing these tissues and cell types derived from these tissues).

The nucleic acids and proteins of the invention are useful in potential therapeutic applications implicated in various diseases and disorders described below and/or other pathologies and disorders. For example, but not limited to, a cDNA encoding the Cortixin-like protein may be useful in gene therapy, and the Cortixin-like protein may be useful when administered to a subject in need thereof. By way of nonlimiting example, the compositions of the present invention will have efficacy for treatment of patients suffering from Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, stroke, tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, cerebral palsy, epilepsy, Lesch-Nyhan syndrome, multiple sclerosis, ataxia-telangiectasia, leukodystrophies, behavioral disorders, addiction, anxiety, pain, memory/perception/attention disorders, and/or neuroprotection. The novel nucleic acid encoding the a Cortixin-like protein, and the a Cortixin-like protein of the invention, or fragments thereof, may further be useful in diagnostic applications, wherein the presence or amount of the nucleic acid or the protein are to be assessed. These materials are further useful in the generation of antibodies that bind immunospecifically to the novel substances of the invention for use in therapeutic or diagnostic methods.

The novel nucleic acid encoding cortixin-like protein, and the cortixin-like protein of the invention, or fragments thereof, may further be useful in diagnostic applications, wherein the presence or amount of the nucleic acid or the protein are to be assessed. These materials are further useful in the generation of antibodies that bind immunospecifically to the novel substances of the invention for use in therapeutic or diagnostic methods. These antibodies may be generated according to methods known in the art, using prediction from hydrophobicity charts, as described in the "Anti-NOVX Antibodies" section below. For example the disclosed NOV5 protein has multiple hydrophilic regions, each of which can be used as an immunogen. In one embodiment, a contemplated NOV5 epitope is from about amino acids 12 to 28. In another embodiment, a NOV5 epitope is from about amino acids 58 to 77. This novel protein also has value in development of powerful assay system for functional analysis of various

human disorders, which will help in understanding of pathology of the disease and development of new drug targets for various disorders.

NOV6

This invention describes novel SN-like proteins, and nucleic acids encoding them, designated 27926453_EXT1 (NOV6). These sequences were initially identified by searching CuraGen's Human SeqCalling database for DNA sequences, which translate into proteins with similarity to a protein family of interest. SeqCalling assembly 27926453_EXT1 was identified as having suitable similarity. SeqCalling assembly 27926453_EXT1 has 1 component. In a search of CuraGen's human expressed sequence assembly database, trimmed assembly s3aq: 27926453 (699 nucleotides) was identified as having homology to this predicted gene sequence (Fig 3B). SeqCalling assembly 27926453_EXT1 was analyzed further to identify open reading frame(s) encoding for a novel full length protein(s) and novel splice forms of these SN. This was done by extending the SeqCalling assembly using suitable additional SeqCalling assemblies, publicly available EST sequences as well public genomic sequence. Public ESTs and additional CuraGen SeqCalling assemblies were identified by the CuraTools™ program SeqExtend. They were included in the DNA sequence extension for SeqCalling assembly 27926453_EXT1 only when sufficient identical overlap was found. These inclusions are described below:

Genomic clone AL109804 was identified as having regions with 100% identity to the SeqCalling assembly 27926453_EXT1 and was selected for analysis. This identity implies that this clone provides the genomic locus for SeqCalling assembly 27926453_EXT1.

The genomic clones were analysed by Genscan and Grail to identify exons and putative coding sequences/open reading frames. This clone was also analyzed by TblastN, BlastX and other homology programs to identify regions translating to proteins with similarity to the original protein/protein family of interest

The results of these analyses were integrated and manually corrected for apparent inconsistencies, thereby obtaining the sequences encoding the full-length protein. When necessary, the process to identify and analyse cDNAs/ESTs and genomic clones was reiterated to derive the full length sequence. This invention describes this full-length DNA sequence and the full-length protein sequence which it encodes. These nucleic acids and protein sequences for each splice form are referred to here as NOV6 (27926453_EXT1).

Specifically, CuraGen's SeqCalling Assembly 27926453_EXT1 is made up of 154 fragments, which are trimmed to a 699 bp contig. SeqCalling Assembly 27926453_EXT1 is found in bone marrow, thyroid, lymph node, pancreas, placenta, fetal liver, heart, prostate, spleen, salivary gland, mammary gland, thalamus, adrenal gland, and kidney. SeqCalling

assembly 27926453_EXT1 showed initial homology, by searching with BLASTX, to a *Mus musculus* (mouse) protein: SIALOADHESIN PRECURSOR (SER) (SWISSNEW-

ACC:Q62230, 1694 aa). Using BlastN, this SeqCalling Assembly was identical at the nucleotide level to a GenBank genomic sequence: GENBANKNEW-ID: HS1009E24|acc:

AL109804 *Homo sapiens* chromosome 20 clone RP5-1009E24,*** SEQUENCING IN

PROGRESS ***, 10 unordered pieces - *Homo sapiens*, 195588 bp. AL109804 was processed

with GenScan and the predicted coding regions were analyzed using BlastX, BlastN and

TBlastN to find exons with homologies to *M. musculus* SN. The genomic clone matched

identically to NOV6. AL109804 was used to extend 27926453_EXT1. This was accomplished

by using the protein sequence of SWISSNEW-ACC:Q62230 and Curatool's TblastN against

the GBNEW database. Intron/exon junctions were determined by manual inspection and corrected

for apparent inconsistencies. BlastX of this sequence showed the correct full-length protein,

27926453_EXT1. The base pair (bp) regions used from the genomic clone were: 179126-

179161, 179532-179912, 180219-180510, 182165-182428, 182802-183053, 184609-184911,

186797-187066, 188129-188455, 188911-189169, 189366-189670, 191333-191596, 191721-

192032, 192554-192806, 193123-193392, 193484-193735, 194054-194358, 140705-140757

which was subsequently corrected for apparent inconsistencies.

The disclosed novel NOV6 nucleic acid of 5103 nucleotides (Accession Number 27926453_EXT1) is shown in Table 6A. An open reading begins with an ATG initiation codon at nucleotides 1-3 and ends with a TGA codon at nucleotides 5101-5103. The start and stop

codons are in bold letters.

Table 6A. NOV6 Nucleotide Sequence (SEQ ID NO:23)

<p>ATGGGCTTCTTGCCCAAGCTTCTCCTCCTGGCCTCAGCCGTTCTTCCCCAGGCCAGGCCTCATGGGGCG TCTCCAGTCCCCAGGACGTGCAGGGTGTGAAGGGTCTTGCTGCTTATCCCCTGCATCTTCAGCTTCCC TGCCGACGTGGAGGTGCCCCGACGGCATCACGCCATCTGGTACTACGACTACTCGGGCCAGCGGCAGGTG GTGAGCCACTCGGCGGACCCCAAGCTGGTGGAGGCCCGCTTCCGCGGCCGCACCGAGTTCATGGGGAACC CCGAGCACAGGGTGTGCAACCTGCTGCTGAAGGACCTGCAGCCGAGGACTCTGGTTCTACAACCTCCG CTTCGAGATCAGTGAGGTCAACCGCTGGTCAGATGTGAAAGGCACCTTGGTCACAGTAACAGGTGATCCC AGGGTGCCCAACATTGCCCTCCCCGGTGGAGCTTCTCGAGGGCACAGAGGTGGACTTCAACTGCTCCACTC CCTACGTATGCCTGCAGGAGCAGGTGACACTGCAGTGGCAAGGCCAGGACCCTGCTCGCTCTGTACCTT CAACAGCCAGAAGTTTGAGCCCAACGGCGTCGGCCACCTGGAGACCCTCCACATGGCCATGTCTCTGGCAG GACCACGGCCGATCCTGCGCTGCCAGCTCTCCGTGGCCAATCACAGGGCTCAGAGCGAGATTACCTCC</p>
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AAGTGAAGTGTGCCCCAAGGGTGTGAAGATCCTCCTCAGCCCTCGGGGAGGAACATCCTTCCAGGTGA
 GCTGGTCACTACTCAGCTGCCAGGTGAACAGCAGCTACCCTGCAGTCAGTTCATTAAAGTGGCTCAAGGAT
 GGGGTACGCCTCCAAACCAAGACTGGTGTGCTGCACCTGCCCCAGGCAGCCTGGAGCGATGCTGGCGTCT
 ACACCTGCCAAGCTGAGAACGGCGTGGGCTCTTTGGTCTCACCCCCATCAGCCTCCACATCTTCGTGGC
 TGAGGTCCAGGTGAGCCAGCAGGTCCCATCCTGGAGAACCAGACAGTGACACTAGTCTGCAACACACCC
 AATGAGGCACCCAGTGATCTCCGCTACAGCTGGTACAAGAACCATGTCCTGCTGGAGGATGCCACTCCC
 ATACCCTCCGGCTGCACTTGGCCACTAGGGCTGATACTGGCTTCTACTTCTGTGAGGTGCAGAACGTCCA
 TGGCAGCGAGCGCTCGGGCCCTGTCAGCGTGGTAGTCACAGACCCGCTCTCACTCCAGTCTGACAGCC
 TTCTGGAGACCCAGCGGGACTTGTGGGCATCCTTCACTGCTCTGTGGTCACTGAGCCCCCTGGCCACAC
 TGGTGTCTGTCACATGGGGTTCATATCCTGGCCTCCACCTCCGGGGACAGTGATCACAGCCCACGCTTCAG
 TGGTACCTCTGGTCCCAACTCCCTGCGCCTGGAGATCCGAGACCTGGAGGAACTGACAGTGGGGAGTAC
 AAGTGCTCAGCCACCAACTCCCTTGGAAATGCAACCTCCACCTGGACTTCCATGCCAATGTGCCCCGTC
 TCCTCATCAGCCCGGCAGCCGAGGTGGTGAAGGACAGGCAGTGACACTGAGCTGCAGAAGCGGCCATAAG
 CCCACACCTGATGCCCGCTTCTCCTGGTACCTGAATGGAGCCTGCTTCACGAGGGTCCCGGCAGCAGC
 CTCTGCTCCCGCGGCTCCAGCACTGACGCCGCTCATACCACTGCCGGGCCGGGACGGCCACAGTG
 CCAGTGGCCCCCTCTCGCCAGCTGTTCTCACTGTGCTCTGTGAGCAGCCACCAGACAACCAACATTCAC
 CACAGGCTGGACCTTGATGCCGCTGGGGCCGGGCTGGACGCGAGGCCTCCTTTGTGCCGTGTGGAC
 AGCGACCCCCCGCCAGGCTGCAGCTGCTCCACAAGGACCGTGTGTGGCCACTTCCCTGCCATCAGGGG
 GTGGCTGCAGCACCTGTGGGGCTGTTCCCCACGCATGAAGGTCAACAAAGCCCCCAACTTGCTGCGTGT
 GGAGATTACAACCCCTTGTGCTGGAAGAGGAGGGCTTGTACCTCTGTGAGGCCAGCAATGCCCTGGGCAAC
 GCCTCCACCTCAGCCACCTTCAATGGCCAGGCCACTGCTCTGGCCATTGCACCATCACACACATTCAGG
 AGGGCAGCAAGCCAACTTGACTTGCAACGTGAGCCGGGAAGCTGCTGGCAGCCCTGCTAACTTCTCCTG
 GTTCCGAAATGGGGTGTGTGGGGCCAGGGTCCCCTGGAGACCGTGACACTGCTGCCCGTGGCCAGAACT
 GATGCTGCCCTTTACGCTGCCGCATCCTGACTGAGGCTGGTGGCCAGCTCTCCACTCCCGTGTCTCTGA
 GTGACTCTATCCCCGGACCGTCCAAAGCTGTGAGCCCTCTAGACATGGGGCCAGGGCCACTGGCTCT
 GTTCATCTGCATGTGGACAGCGCCCCCTGGCCCTTGTCTGGCCCTGTTCCATGGGGAGCACCTCTGGCC
 ACCAGCTGGGTCCCCAGGTCCCATCCCATGGTTCGGTTCAGGCTAAAGCTGAGGCCAACTCCCTGAAGT
 TAGAGGTCCGAGAACTGGGCCTTGGGGACTCTGGCAGCTACCGCTGTGAGGCCACAAATGTTCTTGATC
 ATCCAACACCTCACTCTTCTCCAGGTCCGAGGTGCCTGGGTCCAGGTGTACCATCACCTGAGCTCCAA
 GAGGGCCAGGCTGTGGTCTGAGCTGCCAGGTACACACAGGAGTCCAGAGGGGACCTCATATCGTTGGT
 ATCGGGATGGCCAGCCCCCTCCAGGAGTCGACCTCGGCCAGCTCCGCTTTGCAGCCATACTTTGACACA
 AGCTGGGGCCTATCATTTGCCAAGCCCCAGGCCAGGCTCAGCCACACAGCCTAGCTGACCCATCAGC
 CTCCACGTGTCTGTAAAGGATGCCCCACGCCACGTCACTCACTACCTGATGGACACAGGCCCTGGAC
 GACTGGGCCTCCTCCTGTGCCGTGTGGACAGTGACCTCCGGCCAGCTGCGGCTGCTCCACGGGGATCG
 CTTGTGGCCCTCCACCTACAAGGTGTGGGGGACCCGAAGGCAGCTCTCCAGGCTGCATGTGGCTGTG
 GCCCCAACACACTGCGTCTGGAGATCCACGGGGCTATGCTGGAGGATGAGGGTGTCTATATCTGTGAGG
 CCTCCAACACCCCTGGGGCAGGCCCTCGGCCCTCAGCTGACTTCGACGCTCAAAGCTGTGAATGTGAGGTGT
 GGCCCGGGGCTACCGTGCGGGAGGGGAGCTGGTGAACCTGACCTGCCTTGTGTGGACCACTCACCCGGC
 CCAGCTCACCTACACATGGTACCAGGATGGGCAGCAGCGCCTGGATGCCCACTCCATCCCCCTGCCAAC
 GTCACAGTCAGGGATGCCACCTCCTACCGCTGCGGTGTGGGCCCCCTGGTGGGGACCCCGCCTCTCCA
 GACCTATCACCTTGGACGTCTCACGCGCCCCGCAACCTGCGCTGACCTACCTCCTGGAGAGCCATGGC
 GGGCAGCTGGCCCTGTTACTGTGCACTGTGGACAGCCGCCCCGCGCCAGCTGGCCCTCAGCCACGCCG
 GTCGCCCTCTTGGCCTCCTCGACAGCAGCCTCTGTCCCCAACACCTGCGCTGGAGCTGCGAGGGCCACA
 GCCCAGGGATGAGGGTTTCTACAGCTGCTCTGCCCGCAGCCCTCTGGGCCAGGGCCAAACAGTCCCTGGAG
 CTGCGGCTGGAGGTGCGGGTGATCCTGGCTCCGGAGGCTGCCGTGCTGAAGGTGCCCCCATCACAGTGA
 CCTGTGCGGACCTGCTGCCACGCACCCACACTCTATACTTGGTACCACAACGGTCTGTGGCTGCAGGA
 GGGTCCAGCTGCCTCACTCTCATTCTTGGTGGCCACGCGGGCTCATGCAAGCGCCTACTCTTGGCAGGCC
 CAGGATGCCAGGGCACCCGAGCTCCCGTCTGCTGCCCTGCAAGTCTCTGTGCCCTCAGGACGCTG
 TCCTGTCTCTCTCCGGGACTCCAGGGCCAGATCCATGGCTGTGATACAGTGCACTGTGGACAGTGAGCC
 ACCTGCTGAGCTGGCCCTATCTCATGATGGCAAGGTGCTGGCCACGAGCAGCGGGTCCACAGCTTGGCA
 TCAGGGACAGGCCATGTCCAGGTGGCCCCGAAACGCCCTACGGCTGCAGGTGCAAGATGTGCCTGACAGTG
 ATGACACCTATGTTTGACAGGCCCAAACTTGTCTGGGCTCAATCAGCACCATCGGGCGGTTGACAGGTAGA
 AGGTGAGTGGCGCGTGGTGGCAGAGCCTGGCCTGGACGTGCTGAGGGCGCTGCCCTGAACCTCAGCTGC
 CGCCTCCTGGGTGGCCCTGGGCCTGTGGGCACTCCACCTTTGCATGGTTCTGGAATGACCGGCGGCTGC
 ACGCGGAGCCTGTGCCACTCTCGCCTTACCCACAGTGGCTCGTGCTCAAGCTGGGATGTACCACTGCCT
 GGCTGAGCTCCCCACTGGGGCTGCTGCCCTGCTCCAGTCATGCTCCGTGTGCTCTACCTCCCAAGACG
 CCCACCATGATGGTCTTCTGGAGCCTGAGGGTGGCCTCCGGGGCATCCTGGATTGCCGAGTGACAGCG
 AGCCGCTCGCCAGCCTGACTCTCCACCTTGGCAGTGCAGTGGTGGCCTCCAGTCAGCCCCAGGGTGTCTCC
 TGCAGAGCCACACATCCATGTCTGGCTTCCCCAATGCCCTGAGGGTGGACATCGAGGCGCTGAGGGCC
 AGCGACCAAGGGGAATACATCTGTTCTGCCTCAAATGTCTGGGCCCTGCCTCTACCTCCACCTACTTTG
 GGGTCAGAGCCCTGCACCGCTGCATCAGTTCAGCAGCTGCTCTGGGTCTGGGACTGCTGGTGGCCCT
 CCTGCTCTGCTGTTGGGCTGGGGCCCTGCTACACCTGGAGAAGGAGGCGTGTGTTGAAGCAGAGCATG
 GGCGAGAATCCAGGGCGGGCATCGTCTTTCCATTTACTGCCTCTAGCTGGGTCTTCAAGGTGA

The NOV6 protein encoded by SEQ ID NO:23 has 1700 amino acid residues, and is presented using the one-letter code in Table 6B (SEQ ID NO:24). The SignalP, Psort and/or Hydropathy profile for NOV6a predict that NOV6 has a signal peptide is likely to be localized at the plasma membrane (certainty = 0.4600). NOV6 is also likely to be localized to the

5 endoplasmic reticulum (membrane) (certainty = 0.1000); endoplasmic reticulum (lumen) (certainty = 0.1000); and outside (certainty = 0.1000). The predicted protein is similar to the “SN Family”, some members of which have secreted and membrane localization and can be presented at the plasma membrane. Therefore, it is likely that this novel SN is available at the appropriate subcellular localization and hence accessible for the therapeutic uses described

10 herein. A likely signal peptide cleavage site is indicated at the slash in the sequence GQA-SW, between amino acids 20 and 21 in Table 6B.

Table 6B. Encoded NOV6 protein sequence (SEQ ID NO:24).

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MGFLPKLLLLASAVLPPGQASWGVSSPDVQGVKGSCLLI PCIFSF PADVEVPDGITAIWYYDYSQR
QVVS HSADPKLVEARFRGRTEFMGNPEHRVCNLLKDLQPEDSGSYNFRFEI SEVNRWSDVKGTLVTV
TGDP RVPTIASPVELLEGETEVD FNCSTPYVCLQEQVRLQWQGD PARSVTFNSQKFEPTGVGHLETLH
MAMSWQDHGRILRCQLSVANHRAQSEIHLQVKCAPKGVKILLSPSGRNILPGELVTLTCQVNSSYP AV
SSIKWLKDGVR LQTKTGVLHLPQAAWSDAGVYTCQAENG VGSLSVSPPI SLHIFVAEVQVSPAGPILEN
QTVT LVCNT PNEAPSDLRYSWK NHVLL EDAHSH TLRHLATRADTGFYFCEVQNVHGSESGPVS SV
VTD PPLTPVLTAFLETQAGLVGILHCSVVSEPLATLVLSHG GHI LASTSGDSDHSPRFSGTSGPNSLR
LEIRDLEETDSGEYKCSATNSLGNATSTLDFHANVARLLISPAAEVVEGQAVTLSCRSGLSPTPDARF
SWYLN GALLHEGPGSSLLLPAAST DAGSYHCRARDGHSASGPSPAVLTVLCEQPPRQPTFTTRLDL
DAAGAGARRG LLLCRVDS DFPARLQLLHKDRVATSLPSGGGCSTCGGCSPRMKVT KAPNLLRVEIH
NPLLEEGLYLCEASNALGNASTSATFNGQATVLA IAPSH TLQEGTEANLTCNV SREAAGSPANFSWF
RNGVLWAQGP LETVTLLPVARTDAALYACRILTEAGAQLSTPVLLSVLYPPDRPKLSALLDMGQGHMA
LFICTVDSRPLALLALFHGEHLLATSLGPQVPSHGRFQAKAEANSLKLEVRELGLGDSGSYRCEATNV
LGSSNTSLFFQVRGAWVQVSPSPELQEGQAVVLSCQVHTGVPEGTSYRWRDGGQPLQESTSATLRF AA
ITLTQAGAYHCQAQAPGSATTSLAAPISLHVSKDAPRHVTLTTLMDTGPGRLG LLLCRVDS DFP AQL
RLLHGDR LVASTLQGVGGPEGSSPRLHVAVAPNTLRLEIHGAMLEDEGVYICEASNTLGQASASADFD
AQSC ECAGVARGYRAGGAAGEPDLPCVDHSPGPAHLHMVPGWAAAPGCPLHPPAQRHSQGCHLLPLRC
GPPWSGTPPLQTYHLGRPHAPRNLRLTYLLESHGGQLALVLC TVDSRPPAQLALSHAGRLLASSTAAS
VPNTLRLELRGPQPRDEGFYSCSARSPLGQANTSLELRLEVRVILAPEAAVPEGAPITVTCADPAAHA
PTLYTWYHNGRWLQEGPAASLSFLVATRAHAGAYSCQAQDAQGTRSSRPAALQVLCAPQDAVLSSFRD
SRARMAVIQCTVDSEPPAELALSHDGKVLATSSGVHSLASGTGHVQVARNALRLQVQDVPAGDDTYV
CTAQNLLGSI STIGRLQVEGEWRVVAEPGLDVPEGAALNLSCRL LGPGPGVGNSTFAWFNDRR LHAE
PVPTLAFTHVARAQAGMYHCLAELPTGAAASAPVMLRVLYPPKTPTMMVFVEPEGGLRGILD CRVDSE
PLASLT LHLGSR LVASSQPQGA PAEPHIHVLASPNALRVDIEALRPSDQGEYIC SASNVLG PASTSTY
FGVRALHRLHQFQQLLWVLG LLVGLLLLLLGLGACYTWRRRRRVCKQSMGENPGRASSFHLLPLAGSSR

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The disclosed NOV6 nucleic acid sequence belongs to genomic DNA [Acc.NO.: AL109804 from GenbankNEW]. Within this GenbankNew entry is a note showing that the

15 sequence was from Chromosome 1. Therefore, the likely chromosomal locus of the disclosed NOV6 nucleic acid is Chromosome 1.

NOV6 is expressed in at least the following tissues: bone marrow, thyroid, lymph node, pancreas, placenta, fetal liver, heart, prostate, spleen, salivary gland, mammary gland, thalamus, adrenal gland, and kidney.

The disclosed NOV6 protein (SEQ ID NO:24) has good identity with sialoadhesin proteins. The identity information used for ClustalW analysis is presented in Table 6C.

Table 6C. BLAST results for NOV6					
Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
gi 6919968 sp Q62230 SN MOUSE SIALOADHESIN PRECURSOR (SER); gi 1083506 pir S50065; gi 557254 emb CAA85290.1 ' (Z36293)	Sialoadhesin (<i>Mus musculus</i>)	1694	1097/ 1678 (65%)	1256/1678 (74%) Gaps = 31/1678 (1%)	0.0
gi 13489095 ref NP_075556.1; gi 11493365 emb CAC17543.1 (AL109804)	dJ1009E24.1.1 (sialoadhesin (isoform 1)) (<i>Homo sapiens</i>)	1709	1495/1680 (88%)	1503/1680 (88%) Gaps = 32/1680 (1%)	0.0
gi 557250 emb CAA85 268.1 (Z36233)	sialoadhesin (<i>Mus musculus</i>)	1598	1010/ 1530 (66%)	1153/1530 (75%) Gaps = 31/1530 (2%)	0.0
gi 12656130 gb AAK00757.1 AF230073.1 (AF230073)	sialoadhesin (<i>Homo sapiens</i>)	1709	1494/ 1680 (88%)	1502/1680 (88%) Gaps = 32/1680 (1%)	0.0
gi 10440438 dbj BAB15752.1 (AK024462)	FLJ00055 protein (<i>Homo sapiens</i>)	977	840/955 (87%)	846/955 (87%) Gaps = 16/955 (1%)	0.0
gi 6755584 ref NP_035556.1; gi 2768750 gb AAB95641.1 (U92843)	sialoadhesin (<i>Mus musculus</i>)	1695	1103/ 1678 (75%)	1259/1678 (74%) Gaps = 30/1678 (1%)	0.0
gi 13653900 ref XP_016245.1	sialoadhesin (<i>Homo sapiens</i>)	1620	1422/ 1607 (88%)	1430/1607 (88%) Gaps = 32/1607 (1%)	0.0

gi 11493364 emb CAC17542.1 (AL109804)	dJ1009E24.1.2 (sialoadhesin (isoform 2)) (<i>Homo sapiens</i>)	462	440/445 (98%)	440/445 (98%) Gaps = 2/445 (0%)	0.0
gi 10440432 dbj BAB15749.1 (AK024459); gi 10440472 dbj BAB15769.1 (AK024479)	FLJ00051 protein (<i>Homo sapiens</i>); FLJ00073 protein (<i>Homo sapiens</i>)	462	439/445 (98%)	439/445 (98%) Gaps = 2/445 (0%)	0.0

This information is presented graphically in the multiple sequence alignment given in Table 6D (with NOV6 being shown on line 1) as a ClustalW analysis comparing NOV6 with related protein sequences.

5

Table 6D Information for the ClustalW proteins:

- 1) NOV6 (SEQ ID NO:24)
- 2) gi|6919968| (SEQ ID NO:57)
- 3) gi|13489095| (SEQ ID NO:58)
- 4) gi|557250| (SEQ ID NO:59)
- 5) gi|12656130| (SEQ IDNO:60)

10

	10	20	30	40	50	60	
NOV6	MGFLPKLLLLASAVLPPGOASWGVSSPDVQGVKGSCLLIPCIFSFPADVEVPDGITAIW					
gi 6919968	MCVIFSLLLLASVES-LGQTITWGVSSPKNVQGLSGSCLLIPCIFSYPADVPVSNGITAIW					
gi 13489095	MGFLPKLLLLASFP-AGQASWGVSSPDVQGVKGSCLLIPCIFSFPADVEVPDGITAIW					
gi 557250	MCVIFSLLLLASVES-LGQTITWGVSSPKNVQGLSGSCLLIPCIFSYPADVPVSNGITAIW					
gi 12656130	MGFLPKLLLLASFP-AGQASWGVSSPDVQGVKGSCLLIPCIFSFPADVEVPDGITAIW					
	70	80	90	100	110	120	
NOV6	YYDYSQQRQVVSHSADPKLVEARFRGRTEFMGNPEHRVCNLLKDLQPEDSGSYNFRFEI					
gi 6919968	YYDYSGKRQVVIHSGDPKLVDKRFGRFAELMGNMDHKVCNLLKDLKPEDSGTYNFRFEI					
gi 13489095	YYDYSQQRQVVSHSADPKLVEARFRGRTEFMGNPEHRVCNLLKDLQPEDSGSYNFRFEI					
gi 557250	YYDYSGKRQVVIHSGDPKLVDKRFGRFAELMGNMDHKVCNLLKDLKPEDSGTYNFRFEI					
gi 12656130	YYDYSQQRQVVSHSADPKLVEARFRGRTEFMGNPEHRVCNLLKDLQPEDSGSYNFRFEI					
	130	140	150	160	170	180	
NOV6	SEVNRWSDVKGLTVTVTGDPRVPTIASPVELLEGTEVDFNCSTPYVCLQE-QVRLQWQGG					
gi 6919968	SDSNRWLDVKGTTVTVTDESPPTITIPEETREGMERNFNCSTPYLCLOEKQVSLQWRGG					
gi 13489095	SEVNRWSDVKGLTVTVTGDPRVPTIASPVELLEGTEVDFNCSTPYVCLQE-QVRLQWQGG					
gi 557250	SDSNRWLDVKGTTVTVTDESPPTITIPEETREGMERNFNCSTPYLCLOEKQVSLQWRGG					

gi 12656130	SEVNRWSDVKGLTVTVTEPRVPTIASPVELLEGTEVDENCSTPYVCLQFQVRLQWQGC
	190 200 210 220 230 240
NOV6	DPARSVTFNSOKFEPTGVGHLETLHMAMSWQDHGRILRCQLSVANHRAOSEIHLQVKCAP
gi 6919968	DPTHSVTSSEFQSLPTGSGYHQTTLHMAISWQDHGRITLLCQFSLEGAHSSSRKEVYLQVPHAP
gi 13489095	DPARSVTFNSOKFEPTGVGHLETLHMAMSWQDHGRILRCQLSVANHRAOSEIHLQVKYAP
gi 557250	DPTHSVTSSEFQSLPTGSGYHQTTLHMAISWQDHGRITLLCQFSLEGAHSSSRKEVYLQVPHAP
gi 12656130	DPARSVTFNSQKFEPTGVGHLETLHMAMSWQDHGRILRCQLSVANHRAOSEIHLQVKYAP
	250 260 270 280 290 300
NOV6	KGVKILLSPSGRNILPGELVLTLCQVNSSYPVSSIKWLKDGVRLOTKTGVHLHPQAAWS
gi 6919968	KGVEILLSSSGRNILPGDPVTLTCRVNSSYPAVSAVQWARGVNI GVTGHVLRIFSAAWN
gi 13489095	KGVKILLSPSGRNILPGELVLTLCQVNSSYPVSSIKWLKDGVRLOTKTGVHLHPQAAWS
gi 557250	KGVEILLSSSGRNILPGDPVTLTCRVNSSYPAVSAVQWARGVNI GVTGHVLRIFSAAWN
gi 12656130	KGVKILLSPSGRNILPGELVLTLCQVNSSYPVSSIKWLKDGVRLOTKTGVHLHPQAAWS
	310 320 330 340 350 360
NOV6	DAGVYTCAENGVGSLVSPPISLHIFVAEVQVSPAGPILENQTVTLVCNTFPNEAPSDLRY
gi 6919968	DSCAYTCQATNDMGSLVSSPISLHV FMAEVKMN PAGPVLENETVTLLCSTPKKAPQELRY
gi 13489095	DAGVYTCAENGVGSLVSPPISLHIFMAEVQVSPAGPILENQTVTLVCNTFPNEAPSDLRY
gi 557250	DSCAYTCQATNDMGSLVSSPISLHV FMAEVKMN PAGPVLENETVTLLCSTPKKAPQELRY
gi 12656130	DAGVYTCAENGVGSLVSPPISLHIFMAEVQVSPAGPILENQTVTLVCNTFPNEAPSDLRY
	370 380 390 400 410 420
NOV6	SWYKNHVLLLEDAHSHTLRHLATRADTGFFYFCEVQNVHGSERSGPVSVVVTDPPLTPVLT
gi 6919968	SWYKNHILLEDAHASSTLHLPVATRADTGFFYFCEVQNAQGSERSSELSVVVRYPPPTPDLT
gi 13489095	SWYKNHVLLLEDAHSHTLRHLATRADTGFFYFCEVQNVHGSERSGPVSVVNVNHPPLTPVLT
gi 557250	SWYKNHILLEDAHASSTLHLPVATRADTGFFYFCEVQNAQGSERSSELSVVVRYPPPTPDLT
gi 12656130	SWYKNHVLLLEDAHSHTLRHLATRADTGFFYFCEVQNVHGSERSGPVSVVNVNHPPLTPVLT
	430 440 450 460 470 480
NOV6	AFLETOAGLVGILHCSVVSEPLATLVLSHGHHILASTSGDSDHSPRFSGTSGPNSLRLEI
gi 6919968	TFLETOAGLVGILHCSVVSEPLATVVLSHGGTLTASNSGENDFNPRFRISAPNSLRLEI
gi 13489095	AFLETOAGLVGILHCSVVSEPLATLVLSHGHHILASTSGDSDHSPRFSGTSGPNSLRLEI
gi 557250	TFLETOAGLVGILHCSVVSEPLATVVLSHGGTLTASNSGENDFNPRFRISAPNSLRLEI
gi 12656130	AFLETOAGLVGILHCSVVSEPLATLVLSHGHHILASTSGDSDHSPRFSGTSGPNSLRLEI
	490 500 510 520 530 540
NOV6	RDLEETDSGEYKCSATNSLGNATSTLDFHANVARLLISPAAEVVEGOAVTLSCRGLSPT
gi 6919968	RDLQPADSGEYTC LAVNSLGNSTSSLDIFYANVARLLINFSAEVVEGOAVTLSCRGLSPA
gi 13489095	RDLEETDSGEYKCSATNSLGNATSTLDFHANVARLLISPAAEVVEGOAVTLSCRGLSPT
gi 557250	RDLQPADSGEYTC LAVNSLGNSTSSLDIFYANVARLLINFSAEVVEGOAVTLSCRGLSPA
gi 12656130	RDLEETDSGEYKCSATNSLGNATSTLDFHANVARLLISPAAEVVEGOAVTLSCRGLSPT

	550	560	570	580	590	600
NOV6	PDARFSWYLN	GALLHEGPGSS	LLLPAASSTD	DAGSYHCRARD	GHSASGPSSPA	VLTVICEQ
gi 6919968	PDTREFSWYLN	GALLLEGSS	SSLLLPAASSTD	DAGSYHCRARD	GHSASGPSSPA	VLTVFYP
gi 13489095	PDARFSWYLN	GALLHEGPGSS	LLLPAASSTD	DAGSYHCRARD	GHSASGPSSPA	VLTVLYP
gi 557250	PDTREFSWYLN	GALLLEGSS	SSLLLPAASSTD	DAGSYHCRARD	GHSASGPSSPA	VLTVFYP
gi 12656130	PDARFSWYLN	GALLHEGPGSS	LLLPAASSTD	DAGSYHCRARD	GHSASGPSSPA	VLTVLYP
	610	620	630	640	650	660
NOV6	P	PROPTFTTR	LDLDAAGAG	AGRRGLLL	CRVDS	DPPARLQLLHKDRVVATSLPSGGGCSTC
gi 6919968	-PRK	PTFTARLD	LDLDSGV	CDGRRGI	LLCHVDS	DPPAQLRLHKGHVVATSLP-----SRC
gi 13489095	-P	ROPTFTTR	LDLDAAGAG	AGRRGLLL	CRVDS	DPPARLQLLHKDRVVATSLPSGGGCSTC
gi 557250	-PRK	PTFTARLD	LDLDSGV	CDGRRGI	LLCHVDS	DPPAQLRLHKGHVVATSLP-----SRC
gi 12656130	-P	ROPTFTTR	LDLDAAGAG	AGRRGLLL	CRVDS	DPPARLQLLHKDRVVATSLPSGGGCSTC
	670	680	690	700	710	720
NOV6	GGCSPRMKV	TKAPNLLR	VEIHNP	LEEGLYL	CEASNAL	GNASTSATFNGQATVLAIAPS
gi 6919968	GSCS	ORTKVS	RSTNS	LHVEIQK	PVLE	EGVYLCEASNTLGNSAAASFNAKATVIVITPS
gi 13489095	GGCSPRMKV	TKAPNLLR	VEIHNP	LEEGLYL	CEASNAL	GNASTSATFNGQATVLAIAPS
gi 557250	GSCS	ORTKVS	RSTNS	LHVEIQK	PVLE	EGVYLCEASNTLGNSAAASFNAKATVIVITPS
gi 12656130	GGCSPRMKV	TKAPNLLR	VEIHNP	LEEGLYL	CEASNAL	GNASTSATFNGQATVLAIAPS
	730	740	750	760	770	780
NOV6	HTLQEGTEA	NLCNV	SREAAGS	PANF	SWFRNGVL	WAQGPLETVTLTPVARTDAALYACRI
gi 6919968	N	TLREGTEA	NLCN	GNCEVAV	SPANF	SWFRNGVLWTQGSLETVRQLLARTDAALYACRI
gi 13489095	HTLQEGTEA	NLCNV	SREAAGS	PANF	SWFRNGVL	WAQGPLETVTLTPVARTDAALYACRI
gi 557250	N	TLREGTEA	NLCN	GNCEVAV	SPANF	SWFRNGVLWTQGSLETVRQLLARTDAALYACRI
gi 12656130	HTLQEGTEA	NLCNV	SREAAGS	PANF	SWFRNGVL	WAQGPLETVTLTPVARTDAALYACRI
	790	800	810	820	830	840
NOV6	LTEAGAQL	STPVLL	SVLYPP	DRPKLS	ALLDMGQGH	MAFICTVDSRPLALLALFHGEHLL
gi 6919968	L	TEDGAQL	SAPV	VLSVLYA	DPDPKLS	ALLDVGOGHMAVFICTVDSYPLAHISLFRCHLL
gi 13489095	LTEAGAQL	STPVLL	SVLYPP	DRPKLS	ALLDMGQGH	MAFICTVDSRPLALLALFHGEHLL
gi 557250	L	TEDGAQL	SAPV	VLSVLYA	DPDPKLS	ALLDVGOGHMAVFICTVDSYPLAHISLFRCHLL
gi 12656130	LTEAGAQL	STPVLL	SVLYPP	DRPKLS	ALLDMGQGH	MAFICTVDSRPLALLALFHGEHLL
	850	860	870	880	890	900
NOV6	ATSLGPQV	PSHGRF	OAKAEAN	SLKLEV	RELGLG	DSGSYRCEATNVLGSSNTSLFFQVRGA
gi 6919968	A	TNLEPQR	PSHGRI	OAKATAN	SLCLEV	RELGLVDSGNYHCEATNLGSAANSLFFQVRGA
gi 13489095	ATSLGPQV	PSHGRF	OAKAEAN	SLKLEV	RELGLG	DSGSYRCEATNVLGSSNTSLFFQVRGA
gi 557250	A	TNLEPQR	PSHGRI	OAKATAN	SLCLEV	RELGLVDSGNYHCEATNLGSAANSLFFQVRGA
gi 12656130	ATSLGPQV	PSHGRF	OAKAEAN	SLKLEV	RELGLG	DSGSYRCEATNVLGSSNTSLFFQVRGA

	910	920	930	940	950	960
NOV6	WVQVSPSPPELQEGQAVVLSQVHTGVPEGTSYRWYRDGQPLQESTSATLRFAAITLTQAG				
gi 6919968	WVRFITIT-ELREGQAVVLSQVPTGVSEGTSSYQDGRPLQESTSSTLRIAAISIRQAG				
gi 13489095	WVQVSPSPPELQEGQAVVLSQVHTGVPEGTSYRWYRDGQPLQESTSATLRFAAITLTQAG				
gi 557250	WVRFITIT-ELREGQAVVLSQVPTGVSEGTSSYQDGRPLQESTSSTLRIAAISIRQAG				
gi 12656130	WVQVSPSPPELQEGQAVVLSQVHTGVPEGTSYRWYRDGQPLQESTSATLRFAAITLTQAG				
	970	980	990	1000	1010	1020
NOV6	AYHCQAQAPGSATTSLAAPISLHVSCKDAPRHVTLTTLMDTGPGRLGLLCRVDSPPAQ				
gi 6919968	AYHCQAQAPDIAIASLAAPVSLHVS--YTPRHVTLTTLMDTGPGRLGLLCRVDSPPAQ				
gi 13489095	AYHCQAQAPGSATTSLAAPISLHVS--YAPRHVTLTTLMDTGPGRLGLLCRVDSPPAQ				
gi 557250	AYHCQAQAPDIAIASLAAPVSLHVS--YTPRHVTLTTLMDTGPGRLGLLCRVDSPPAQ				
gi 12656130	AYHCQAQAPGSATTSLAAPISLHVS--YAPRHVTLTTLMDTGPGRLGLLCRVDSPPAQ				
	1030	1040	1050	1060	1070	1080
NOV6	LRLHGDRLVASTLQGVGGPEGSSPRLHVAVAPNTRLRLEIHGAMLEDEGVYICEASNTLG				
gi 6919968	LQLFHRNRLVASTLQCADELAGSNPRLHVTVLPNELRLQIHFPPELEDQTYTCEASNTLG				
gi 13489095	LRLHGDRLVASTLQGVGGPEGSSPRLHVAVAPNTRLRLEIHGAMLEDEGVYICEASNTLG				
gi 557250	LQLFHRNRLVASTLQCADELAGSNPRLHVTVLPNELRLQIHFPPELEDQTYTCEASNTLG				
gi 12656130	LRLHGDRLVASTLQGVGGPEGSSPRLHVAVAPNTRLRLEIHGAMLEDEGVYICEASNTLG				
	1090	1100	1110	1120	1130	1140
NOV6	QASASADFDAQSCCEAGVARGYRAGCAAGEPDLPCVDHSPGPAHLHMPGWAAPGCPLH				
gi 6919968	QASAAADFDAQAVRVTVWPNATVQEGQVNLTCVWSTHQDSLSTYTWYKGGQOLGARS				
gi 13489095	QASASADFDAQAVNVQVWEGATVREGQLVNLTCVWSTHPAQITYTWYQDGOORIDAHSI				
gi 557250	QASAAADFDAQAVRVTVWPNATVQEGQVNLTCVWSTHQDSLSTYTWYKGGQOLGARS				
gi 12656130	QASASADFDAQAVNVQVWEGATVREGQLVNLTCVWSTHPAQITYTWYQDGOORIDAHSI				
	1150	1160	1170	1180	1190	1200
NOV6	PPAQRHSQGGCHLLPLRCGPFWSGTPPLQTYHIGRPHAPRNLRLTYLLESHGGQALVLCT				
gi 6919968	TLPSSVKVL DATSYRCGVGLPCHAPHLSRPITLDVLHAPRNLRLTYLLETCGRQLALVLCT				
gi 13489095	PLPNVTVR DATSYRCGVGPPGRAPRLSRPITLDVLHAPRNLRLTYLLESHGGQALVLCT				
gi 557250	TLPSSVKVL DATSYRCGVGLPCHAPHLSRPITLDVLHAPRNLRLTYLLETCGRQLALVLCT				
gi 12656130	PLPNVTVR DATSYRCGVGPPGRAPRLSRPITLDVLHAPRNLRLTYLLESHGGQALVLCT				
	1210	1220	1230	1240	1250	1260
NOV6	VDSRPPAQLALSHAGRLASSTAASVPNTLRLELRGPQPRDEGFYSCSARSPLGQANTSL				
gi 6919968	VDSRPPAQLTLSHGDLVASSTEASVPNTLRLEIQDPRPSNEGLYSCSAHSPLGKANTSL				
gi 13489095	VDSRPPAQLALSHAGRLASSTAASVPNTLRLELRGPQPRDEGFYSCSARSPLGQANTSL				
gi 557250	VDSRPPAQLTLSHGDLVASSTEASVPNTLRLEIQDPRPSNEGLYSCSAHSPLGKANTSL				
gi 12656130	VDSRPPAQLALSHAGRLASSTAASVPNTLRLELRGPQPRDEGFYSCSARSPLGQANTSL				
	1270	1280	1290	1300	1310	1320

NOV6	ELRLLE-VRVILAPEAAVPEGAPITVTCADPAAHAPTLYTWYHNGRWLQEGPAASLSFLVA
gi 6919968	ELRLLEGVRVKMNPSCSVPEGEFVTVTCEDPAALSSALYAWFHNGHWLQEGPASLSQLFLT
gi 13489095	ELRLLEGVRVILAPEAAVPEGAPITVTCADPAAHAPTLYTWYHNGRWLQEGPAASLSFLVA
gi 557250	ELRLLEGVRVKMNPSCSVPEGEFVTVTCEDPAALSSALYAWFHNGHWLQEGPASLSQLFLT
gi 12656130	ELRLLEGVRVILAPEAAVPEGAPITVTCADPAAHAPTLYTWYHNGRWLQEGPAASLSFLVA
	1330 1340 1350 1360 1370 1380
NOV6	TRAHAGAYSCQAQDAQGTRSSRPAALQVLCAPQDAVLSSFRDSRARSMAVIQCTVDSEPP
gi 6919968	TRAHAGAYFCQVHDTQGRSSRPAALQVLYAPQDAVLSSFRDSRTRLMVVIQCTVDSEPP
gi 13489095	TRAHAGAYSCQAQDAQGTRSSRPAALQVLYAPQDAVLSSFRDSRARSMAVIQCTVDSEPP
gi 557250	TRAHAGAYFCQVHDTQGRSSRPAALQVLYAPQDAVLSSFRDSRTRLMVVIQCTVDSEPP
gi 12656130	TRAHAGAYSCQAQDAQGTRSSRPAALQVLYAPQDAVLSSFRDSRARSMAVIQCTVDSEPP
	1390 1400 1410 1420 1430 1440
NOV6	AELALSHDGKVLATSSGVHSLASGTGHVQVARNALRLQVQDVPAGD-DTYVCTAQNLLGS
gi 6919968	AELVLSHNGKVLAAASHERHSSASGIGHIQVARNALRLQVQDVTLDGNTYVCTAQTTLGS
gi 13489095	AELALSHDGKVLATSSGVHSLASGTGHVQVARNALRLQVQDVPAGD-DTYVCTAQNLLGS
gi 557250	AELVLSHNGKVLAAASHERHSSASGIGHIQVARNALRLQVQDVTLDGNTYVCTAQTTLGS
gi 12656130	AELALSHDGKVLATSSGVHSLASGTGHVQVARNALRLQVQDVPAGD-DTYVCTAQNLLGS
	1450 1460 1470 1480 1490 1500
NOV6	ISTIGRLQVEGEWRVVAEPGLDVPEGAALNLSCLLGGPGPGVGNSTFAFWNDRRLHAEP
gi 6919968	ISTIGRLQVEGEWRVVAEPGLDVPEGAALNLSCLLGGPGPGVGNSTFAFWNDRRLHAEP
gi 13489095	ISTIGRLQVEGEWRVVAEPGLDVPEGAALNLSCLLGGPGPGVGNSTFAFWNDRRLHAEP
gi 557250	ISTIGRLQVEGEWRVVAEPGLDVPEGAALNLSCLLGGPGPGVGNSTFAFWNDRRLHAEP
gi 12656130	ISTIGRLQVEGEWRVVAEPGLDVPEGAALNLSCLLGGPGPGVGNSTFAFWNDRRLHAEP
	1510 1520 1530 1540 1550 1560
NOV6	VPTLAFTHVARAQAGMYHCLAEPLTGAAASAPVMLRVLYPPKTPPTMMVFVEPEGGLRGIL
gi 6919968	VPTLSFTFVVRQAAGLYHCRADLPTGATTAPVMLRVLYPPKTPPTLIVFVEPEGGLRGIL
gi 13489095	VPTLAFTHVARAQAGMYHCLAEPLTGAAASAPVMLRVLYPPKTPPTMMVFVEPEGGLRGIL
gi 557250	VPTLSFTFVVRQAAGLYHCRADLPTGATTAPVMLRVLYPPKTPPTLIVFVEPEGGLRGIL
gi 12656130	VPTLAFTHVARAQAGMYHCLAEPLTGAAASAPVMLRVLYPPKTPPTMMVFVEPEGGLRGIL
	1570 1580 1590 1600 1610 1620
NOV6	DCRVDSEPLASLTLLHLSRLVASSOPQGAPEPHIHVLASPNALRVDIEALRPSDQGEYI
gi 6919968	DCRVDSEPLAITLLHLSRLVASSOPQGAPEPHIHVLASPNALRVDIEALRPSDQGEYI
gi 13489095	DCRVDSEPLASLTLLHLSRLVASSOPQGAPEPHIHVLASPNALRVDIEALRPSDQGEYI
gi 557250	-----LHH-----
gi 12656130	DCRVDSEPLASLTLLHLSRLVASSOPQGAPEPHIHVLASPNALRVDIEALRPSDQGEYI
	1630 1640 1650 1660 1670 1680

NOV6	CSASNVLG ¹⁶⁹⁰ PASTSTYFGVRLHRLHQFQQLLWVLG ¹⁷⁰⁰ LLVGL ¹⁷¹⁰ LLLLLGLGACYTWRRRRVCK
gi 6919968	CTASNTLGSASAS ¹⁶⁹⁰ YFGTRALHQLQ ¹⁷⁰⁰ IFORLLWVLG ¹⁷¹⁰ FLAGFLCLLLGLVYHTWRKKSS ¹⁷²⁰ TK
gi 13489095	CSASNVLGSASTSTYFGVRLHRLHQFQQLLWVLG ¹⁶⁹⁰ LLVGL ¹⁷⁰⁰ LLLLLGLGACYTWRRRRVCK
gi 557250	TGPYQAFSSA ¹⁶⁹⁰ QSKGE ¹⁷⁰⁰ ICKGLRTLASSLAGC ¹⁷¹⁰ WVFS ¹⁷²⁰ MLGYPA ¹⁷³⁰ IKWRI ¹⁷⁴⁰ LLPF ¹⁷⁵⁰ WDEY ¹⁷⁶⁰ RF----
gi 12656130	CSASNVLGSASTSTYFGVRLHRLHQFQQLLWVLG ¹⁶⁹⁰ LLVGL ¹⁷⁰⁰ LLLLLGLGACYTWRRRRVCK
<div> <div>169017001710</div> <div>....</div> </div>	
NOV6	QSMGEN-----PGRASSFHL ¹⁶⁹⁰ FLAG ¹⁷⁰⁰ SSR-----
gi 6919968	L ¹⁶⁹⁰ NEDENSAEMAT ¹⁷⁰⁰ KNTI ¹⁷¹⁰ QEEVVAAL-----
gi 13489095	QSMGENSVEMAFQNET ¹⁶⁹⁰ IT ¹⁷⁰⁰ QL ¹⁷¹⁰ ED ¹⁷²⁰ PD ¹⁷³⁰ AA ¹⁷⁴⁰ TCETSTCAPPLG
gi 557250	-----
gi 12656130	QSMGENSVEMAFQNET ¹⁶⁹⁰ IT ¹⁷⁰⁰ QL ¹⁷¹⁰ ED ¹⁷²⁰ PD ¹⁷³⁰ AA ¹⁷⁴⁰ TCETSTCAPPLG

The presence of identifiable domains in NOV6 was determined by searches using algorithms such as PROSITE, Blocks, Pfam, ProDomain, Prints and then determining the Interpro number by crossing the domain match (or numbers) using the Interpro website (<http://www.ebi.ac.uk/interpro/>).

DOMAIN results for NOV6 were collected from the Conserved Domain Database (CDD) with Reverse Position Specific BLAST. This BLAST samples domains found in the Smart and Pfam collections. The results are listed in Table 6E with the statistics and domain description. The results indicate that this protein contains at least one immunoglobulin domain.

The presence of these identifiable domains is shown in Table 6F.

Table 6E. Domain Results for NOV6

Domain Identifier	Domain Name	Score (Bits)	E Value
gnl Smart IG	Immunoglobulin	<u>53.1</u>	1e-07
gnl Smart IG	Immunoglobulin	<u>48.5</u>	3e-06
gnl Smart IG	Immunoglobulin	<u>43.9</u>	7e-05
gnl Smart IG	Immunoglobulin	<u>40.0</u>	0.001
gnl Smart IG	Immunoglobulin	<u>38.9</u>	0.002
gnl Smart IG	Immunoglobulin	<u>38.9</u>	0.002
gnl Smart IG	Immunoglobulin	<u>37.4</u>	0.006
gnl Smart IG_like	Immunoglobulin like; IG domains that cannot be classified into...	<u>52.8</u>	1e-07
gnl Smart IG_like	Immunoglobulin like; IG domains that cannot be classified into...	<u>50.1</u>	1e-06
gnl Smart IG_like	Immunoglobulin like; IG domains that cannot be classified into...	<u>47.4</u>	6e-06

<u>gnl Smart IG_like</u>	Immunoglobulin like; IG domains that cannot be classified into...	<u>43.9</u>	7e-05
<u>gnl Smart IG_like</u>	Immunoglobulin like; IG domains that cannot be classified into...	<u>41.6</u>	3e-04
<u>gnl Smart IG_like</u>	Immunoglobulin like; IG domains that cannot be classified into...	<u>40.8</u>	6e-04
<u>gnl Smart IG_like</u>	Immunoglobulin like; IG domains that cannot be classified into...	<u>39.3</u>	0.002
<u>gnl Smart IG_like</u>	Immunoglobulin like; IG domains that cannot be classified into...	<u>38.5</u>	0.003
<u>gnl Smart IG_like</u>	Immunoglobulin like; IG domains that cannot be classified into...	<u>38.1</u>	0.004
<u>gnl Smart IG_like</u>	Immunoglobulin like; IG domains that cannot be classified into...	<u>37.7</u>	0.005
<u>gnl Smart IG_like</u>	Immunoglobulin like; IG domains that cannot be classified into...	<u>37.7</u>	0.005
<u>gnl Smart IG_like</u>	Immunoglobulin like; IG domains that cannot be classified into...	<u>37.7</u>	0.005
<u>gnl Smart IG_like</u>	Immunoglobulin like; IG domains that cannot be classified into...	<u>37.7</u>	0.005
<u>gnl Smart IGc2</u>	Immunoglobulin C-2 Type	<u>38.9</u>	0.002
<u>gnl Pfam pfam00047</u>	Ig, Immunoglobulin domain	<u>37.7</u>	0.005
<u>gnl Pfam pfam00047</u>	Ig, Immunoglobulin domain	<u>37.4</u>	0.006

Table 6F. DOMAIN results for NOV6

<u>gnl Smart IG, Immunoglobulin</u>			
CD-Length = 63 residues, 100.0% aligned			
Score = 53.1 bits (126), Expect = 1e-07			
Query: 254	LPGELVTLTQVNSSYPVSSIKWLKDGVRQLQ-----TKTGVLHLPQAAWSAGVYTCQA	308	
Sbjct: 1	LEGESVTLTCPASGDPVP--NITWLKDGKPLPESRVVASGSTLTIKNVSLEDSGLYTCVA	58	
Query: 309	ENGVG 313 (SEQ ID NO:109)		
Sbjct: 59	RNSAG 63 (SEQ ID NO:110)		
<hr/>			
<u>gnl Smart IG, Immunoglobulin</u>			
CD-Length = 63 residues, 93.7% aligned			
Score = 48.5 bits (114), Expect = 3e-06			
Query: 910	QEGQAVVLSQVHTGVPEGTSYRWYRDGQPLQES----TSATLRFAAITLTQAGAYHCQA	965	
Sbjct: 1	LEGESVTLTCPA-SGDPVPN-ITWLKDGKPLPESRVVASGSTLTIKNVSLEDSGLYTCVA	58	
Query: 966	Q 966 (SEQ ID NO:111)		
Sbjct: 59	R 59 (SEQ ID NO:112)		
<hr/>			
<u>gnl Smart IG, Immunoglobulin</u>			
CD-Length = 63 residues, 98.4% aligned			
Score = 43.9 bits (102), Expect = 7e-05			
Query: 1277	EGAPITVTCADPAAHAPTLYTWYHNGRWLQEGPA-----ASLSFLVATRAHAGAYSCQAQD	1332	
Sbjct: 2	EGESVTLTCPASGDPVPNI-TWLKDGKPLPESRVVASGSTLTIKNVSLEDSGLYTCVARN	60	

Query: 1333 AQG 1335 (SEQ ID NO:113)
 Sbjct: 61 SAG 63 (SEQ ID NO:114)

gnl|Smart|IG, Immunoglobulin

CD-Length = 63 residues, 100.0% aligned
 Score = 40.0 bits (92), Expect = 0.001

Query: 338 LENQTVTLVCN-TPNEAPSDLRYSWYKNHVLLLEDAHSH----TLRLHLATRADTGFFYFCE 392
 Sbjct: 1 LEGESVTLTCPASGDPVPN---ITWLKDGKPLPESRVVASGSTLTIKNVSLEDSGLYTCV 57

Query: 393 VQNVHG 398 (SEQ ID NO:115)
 Sbjct: 58 ARNSAG 63 (SEQ ID NO:116)

gnl|Smart|IG, Immunoglobulin

CD-Length = 63 residues, 98.4% aligned
 Score = 38.9 bits (89), Expect = 0.002

Query: 1462 EGAALNLSCLLGGPGPVGNSTFAWFWNDRRLHAEPV----PTLAFTHVARAQAGMYHCL 1517
 Sbjct: 2 EGESVTLTCPASGDPVPN---NITWLKDGKPLPESRVVASGSTLTIKNVSLEDSGLYTCV 57

Query: 1518 AELPTG 1523 (SEQ ID NO:117)
 Sbjct: 58 ARNSAG 63 (SEQ ID NO:118)

gnl|Smart|IG, Immunoglobulin

CD-Length = 63 residues, 98.4% aligned
 Score = 38.9 bits (89), Expect = 0.002

Query: 524 EGQAVTLSCRSGLSPTPDARFSWYLNALLHE----GPGSSLLLPAASSTDAGSYHCRAR 579
 Sbjct: 2 EGESVTLTCPASGDPVPN--ITWLKDGKPLPESRVVASGSTLTIKNVSLEDSGLYTCVAR 59

Query: 580 DGHS 583 (SEQ ID NO:119)
 Sbjct: 60 NSAG 63 (SEQ ID NO:120)

gnl|Smart|IG, Immunoglobulin

CD-Length = 63 residues, 100.0% aligned
 Score = 37.4 bits (85), Expect = 0.006

Query: 723 QEGTEANLTCNVSREAAGSP-ANFSWRNGVLWAQGPLE----TVTLLPVARTDAALYAC 777
 Sbjct: 1 LEGESVTLTC----PASGDPVPNITWLKDGKPLPESRVVASGSTLTIKNVSLEDSGLYTC 56

Query: 778 RILTEAG 784 (SEQ ID NO:121)
 Sbjct: 57 VARNSAG 63 (SEQ ID NO:122)

gnl|Smart|IG like, Immunoglobulin like; IG domains
 that cannot be classified into one of IGv1, IGc1, IGc2, IG.

CD-Length = 86 residues, 93.0% aligned
 Score = 52.8 bits (125), Expect = 1e-07

Query: 248 PSGRNILPGELVTLTCQVNSSYPVAVSSIKWLKDG-----VRLQTKTGVLHLPQA 296
 Sbjct: 1 PPSVTVKEGESVTLSCASGNPPP--TVTWYKQGGKLLAESGRFSVSRSGGNSTLTISNV 58

Query: 297 AWS DAGVYTCQAENGVGSLVSP 318 (SEQ ID NO:123)
 Sbjct: 59 TPEDSGTYTCAATNGSGSASSG 80 (SEQ ID NO:124)

gnl|Smart|IG like, Immunoglobulin like; IG domains
 that cannot be classified into one of IGv1, IGc1, IGc2, IG.

CD-Length = 86 residues, 77.9% aligned
 Score = 50.1 bits (118), Expect = 1e-06

Query: 432 LHCSVVSEPLATLVLSHGHHILASTSGDSDHSPRFSGTSGPNSLRLEIRDLEETDSGEYK 491
 Sbjct: 14 LSCEASGNPPPTVTWYKQGGKLLAESG-----RFSVSRSGGNSTLTISNVTPEDSGTYT 67

Query: 492 CENLNGSLNAT86 residue 180 NO:125igned
 Sbjct: 68 SCRAATNGSGSASSG 80 (SEQ ID NO:126)
 Query: 904 SPSPQLQEGQAVVLSCQVHTGVPEGTSYRWYRDGQPL-----QESTSATLRFAAI 953
 Sbjct: 1 PPSVTVKEGESVTLSCFA-SGNPP-PTVTWYKOGGKLLAESGRFSVSRSGGNSTLTISNV 58

Query: 934 TLTAAGAYHCOAAGSATTSLAAPISLHVS (SEQ ID NO:131)
 Sbjct: 59 CDPEBSGTHTEAAT-RENCGGASSGVTLVWLa186 (SEQ ID NO:132)
 Score = 47.4 bits (111), Expect = 6e-06
 Cn-length: 86 residue 180 aligned
 Query: 339 SCRAATNGSLNAT86 residue 180 NO:125igned 388
 Sbjct: 8 SCRAATNGSGSASSG 80 (SEQ ID NO:126)
 Query: 1008 LLCRVDSDPFAQLRLLHGDRLVASTLQGVGGPEGSSPRLHVAVAPNTRLRLEIHGAMLEDE 1067
 Sbjct: 14 LSCAASGNRPPTVTWYKOG 403 (SEQ ID NO:127)
 Query: 389 YFCEVQNVHGSERSG 403 (SEQ ID NO:127)
 Sbjct: 66 YTCAATNGSGSASSG 80 (SEQ ID NO:128)
 Query: 1068 GVIICEASNTLG 1079 (SEQ ID NO:129)
 Sbjct: 64 GTYTCAATNGSG 75 (SEQ ID NO:130)

that cannot be classified into one of IGv1, IGc1, IGc2, IG.

CD-Length = 86 residues, 86.0% aligned

Score = 38.5 bits (88), Expect = 0.003

Query: 1275 VPEGAPITVTCADPAAHAPTLYTWYHNG-----RWLQEGPAASLSFLVATRAHAG 1324
Sbjct: 6 VKEGESVTLSCASGNPPPTV-TWYKQGGKLLAESGRFSVSRSGGNSTLTISNVTPEDSG 64

Query: 1325 AYSCQAQDAQGTRSS 1339 (SEQ ID NO:137)

Sbjct: 65 TYTCAATNGSGSASS 79 (SEQ ID NO:138)

gnl|Smart|IG like, Immunoglobulin like; IG domains

that cannot be classified into one of IGv1, IGc1, IGc2, IG.

CD-Length = 86 residues, 98.8% aligned

Score = 38.1 bits (87), Expect = 0.004

Query: 718 PSHTLQEGTEANLTCNVSREAAAGSPANFWSFRNGVLWAQGPLE-----TVTLLPV 767
Sbjct: 2 PSVTVKEGESVTLSCAS---GNPPPTVTWYKQGGKLLAESGRFSVSRSGGNSTLTISNV 58

Query: 768 ARTDAALYACRILTEAGAQLSTPVLSSVL 796 (SEQ ID NO:139)

Sbjct: 59 TPEDSGTYTCAATNGSG-SASSGVTLTVL 86 (SEQ ID NO:140)

gnl|Smart|IG like, Immunoglobulin like; IG domains

that cannot be classified into one of IGv1, IGc1, IGc2, IG.

CD-Length = 86 residues, 77.9% aligned

Score = 37.7 bits (86), Expect = 0.005

Query: 627 CRVDSPPARLQLLHKDRVATSLPSGGGCSTCGGCSFRMKVTKAPNLLRVEIHNPPLLE 686
Sbjct: 16 CEASGNPPPTVTWYKQGGKLLAE-----SGRFSVSRSGGNSTLTISNVTPE 62

Query: 687 EGLYLCEASNALGNASTSAT 706 (SEQ ID NO:141)

Sbjct: 63 SGTYTCAATNGSGSASSGV 82 (SEQ ID NO:142)

gnl|Smart|IG like, Immunoglobulin like; IG domains

that cannot be classified into one of IGv1, IGc1, IGc2, IG.

CD-Length = 86 residues, 79.1% aligned

Score = 37.7 bits (86), Expect = 0.005

Query: 1557 LDCRVDSPLASLTLHLGSRVLVASSQPQGAPEPHIVLASPNALRVDIEALRPSDQGEY 1616
Sbjct: 14 LSCEASGNPPPTVTWYKQG-----GKLLAESGRFSVSRSGGNSTLTISNVTPEDSGT 66

Query: 1617 ICSASNVLGPASTST 1631 (SEQ ID NO:143)

Sbjct: 67 TCAATNGSGSASSGV 81 (SEQ ID NO:144)

gnl|Smart|IG like, Immunoglobulin like; IG domains

that cannot be classified into one of IGv1, IGc1, IGc2, IG.

CD-Length = 86 residues, 89.5% aligned

Score = 37.7 bits (86), Expect = 0.005

Query: 813 GHMALFICTVDSRPLALLALFHGEHLLATSLGPQVPSHGRFQAKAEANSLKLEVRELGLG 872
Sbjct: 9 GESVTLSCASGNPPPTVTWYKQG-----GKLLAESGRFSVSRSGGNSTLTISNVTPE 61

Query: 873 DSGSYRCEATNVLGSSNTSLFFQV 896 (SEQ ID NO:145)

Sbjct: 62 DSGTYTCAATNGSGSASSGVTLTV 85 (SEQ ID NO:146)

gnl|Smart|IG like, Immunoglobulin like; IG domains

that cannot be classified into one of IGv1, IGc1, IGc2, IG.

CD-Length = 86 residues, 94.2% aligned

Score = 37.7 bits (86), Expect = 0.005

Query: 1460 VPEGAALNLSRLLGGPGPVGNSTFAWFNDRLHAEP-----VPTLAFTHVARA 1509
Sbjct: 6 VKEGESVTLSCASGNPPP---TVTWYKQGGKLLAESGRFSVSRSGGNSTLTISNVTPE 61

Query: 1510 QAGMYHCLAEPLTGAAASAPVMLRVL 1535 (SEQ ID NO:147)

Sbjct:	62	DSGTYTCAAT-NGSGSASSGVTLTVL	86 (SEQ ID NO:148)
<hr/>			
gnl Smart IGc2, Immunoglobulin C-2 Type			
CD-Length = 74 residues, 89.2% aligned			
Score = 38.9 bits (89), Expect = 0.002			
Query:	259	VTLTCQVNSSYP AVSSIKWLKDG VRLQTKTG-----VLHLPQA AWS DAG	302
Sbjct:	2	ATLVCLVTGFYPPDITVTWLKNGQEV TSGVETTDPLKEK DGTYSLSYLTVS-ATWESGD	60
Query:	303	VYTCQAE	309 (SEQ ID NO:149)
Sbjct:	61	TYTCRVT	67 (SEQ ID NO:150)
<hr/>			
gnl Pfam pfam00047, ig, Immunoglobulin domain.			
CD-Length = 68 residues, 100.0% aligned			
Score = 37.7 bits (86), Expect = 0.005			
Query:	256	GELVTLTCQVNSSYP AVSSIKWLKDG VRLQTKTG-----LHLPQA AWS	299
Sbjct:	1	GESVTLTCSV-SGYPPDPTVTWLRNGK GIELLGSSSRVTSGGRFSISSLSLT ISSVTPE	59
Query:	300	DAGVYTCQA	308 (SEQ ID NO:151)
Sbjct:	60	DSGTYTCVV	68 (SEQ ID NO:152)
<hr/>			
gnl Pfam pfam00047, ig, Immunoglobulin domain.			
CD-Length = 68 residues, 100.0% aligned			
Score = 37.4 bits (85), Expect = 0.006			
Query:	340	NQTVTLVCNTPNEAPSDLRYSWYKNHV LLE-----DAHSHTLR LHLATRA	384
Sbjct:	1	GESVTLTCSVSG-YPPDPTVTWLRNGK GIELLGSSSRVTSGGRFSISSLSLT ISSVTPE	59
Query:	385	DTGFYFCEV	393 (SEQ ID NO:153)
Sbjct:	60	DSGTYTCVV	68 (SEQ ID NO:154)

Other BLAST results include sequences from the Patp database, which is a proprietary database that contains sequences published in patents and patent publications. Patp results include those listed in Table 6G.

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Table 6G. Patp alignments of NOV6			
Sequences producing High-scoring Segment Pairs:			Smallest
			Sum
	Reading	High	Prob.
	Frame	Score	P (N)
Patp:AAB41901 Human ORFX polypeptide sequence, 235 aa	+1	1217	8.1e-123

For example, a BLAST against patp: AAB41901, a 235 amino acid Human ORFX polypeptide sequence (WO/0058473), produced good identity, $E = 8.1e-123$ over the region from amino acid 3 to amino acid 235.

Crocker et.al., EMBO J 10(7):1661-69 (1991); PMID: 2050106, UI: 91266893, examined macrophage subpopulations in the mouse that express a lectin-like receptor, sialoadhesin (originally named sheep erythrocyte receptor ("SER")), which selectively recognizes sialoglyco-conjugates and is likely to be involved in cellular interactions of stromal macrophages in haematopoietic and lymphoid tissues. Crocker et al. further described the purification and ligand specificity of sialoadhesin isolated from mouse spleen. Purified sialoadhesin, a glycoprotein of 185 kd apparent Mw, agglutinated sheep or human erythrocytes at nanomolar concentrations in a sialic acid-dependent manner. Low angle shadowing and electron microscopy showed that sialoadhesin consists of a globular head region of approximately 9 nm and an extended tail of approximately 35 nm.

To investigate the specificity for sialic acid, the interaction of sialoadhesin with derivatized human erythrocytes, glycoproteins, and glycolipids was examined. Sialoadhesin specifically recognizes the oligosaccharide sequence Neu5Ac alpha 2----3Gal beta 1----3GalNAc in either sialoglycoproteins or gangliosides. These findings imply that specific sialoglycoconjugates carrying this structure may be involved in cellular interactions between stromal macrophages and subpopulations of haematopoietic cells and lymphocytes.

The extracellular region of sialoadhesin is composed of seventeen immunoglobulin-like domains, of which the amino-terminal two are highly-related structurally and functionally to the amino-terminal domains of CD22, myelin associated glycoprotein and CD33. These proteins, collectively known as the sialoadhesin family, are able to mediate sialic acid-dependent binding with distinct specificities for both the type of sialic acid and its linkage to subterminal sugars.

Additionally, Crocker et.al. (Glycoconj J 14(5):601-09 (1997)) reviewed their recent studies on sialoadhesin and suggested how this molecule may contribute to a range of macrophage functions, both under normal conditions as well as during inflammatory reactions. (See also, Crocker et.al., EMBO J 13(19):4490-503 (1994), which reports the molecular cloning of murine sialoadhesin and show that it is a new member of the immunoglobulin (Ig) superfamily with 17 Ig-like domains. COS cells transfected with a cDNA encoding full-length sialoadhesin bound mouse bone marrow cells in a sialic acid-dependent manner). Alternatively spliced cDNAs, predicting soluble forms of sialoadhesin containing the first three or 16 Ig-like domains of sialoadhesin, were expressed in COS cells and the respective proteins purified. When immobilized on plastic, the 16-domain form bound cells in a sialic acid-dependent manner, suggesting that sialoadhesin can function in both secreted and membrane-bound forms.

The most similar proteins in the database were CD22, myelin-associated glycoprotein, Schwann cell myelin protein and CD33. Like sialoadhesin, CD22 mediates sialic acid-dependent cell adhesion. The sequence similarity of sialoadhesin to CD22 and related members of the Ig superfamily indicates the existence of a novel family of sialic acid binding proteins involved in cell-cell interactions.

Stromal macrophages in lymphohemopoietic tissues express novel macrophage-restricted plasma membrane receptors involved in nonphagocytic interactions with other hemopoietic cells. One such receptor with lectin-like specificity for sialylated glycoconjugates on sheep erythrocytes and murine hemopoietic cells has been characterized immunochemically and termed sialoadhesin. Sialoadhesin expression during mouse development was examined to learn more about its regulation and function. See Morris et.al., Dev Immunol 2(1):7-17 (1992). PMID: 1521065, UI: 92393348. Immunocytochemical, rosetting, and Western blot studies show that sialoadhesin is first detected on fetal liver macrophages on day 18 of development, 7 days after numerous F4/80+ macrophages are found within erythroblastic islands. In spleen and bone marrow, sialoadhesin appears between day 18 and birth, in parallel with myeloid development. Strongly labeled macrophages in the marginal zone of spleen, characteristic of adult lymphoid tissues, appeared gradually between 1-4 weeks after birth, as the white pulp became enlarged. Isolation of fetal liver macrophages at day 14 confirmed that sialoadhesin was not involved in the binding of erythroblasts, which is mediated by a distinct cation-dependent receptor.

Sialoadhesin could be expressed by isolated fetal liver macrophages after cultivation in adult mouse serum, a known source of inducer activity, but was not dependent on the presence of this inducer, unlike adult-derived macrophages. Fetal plasma contained inducing activity on day 13, but adult levels were not reached until 2 weeks postnatally. These studies show that sialoadhesin is differentially regulated compared with the erythroblast receptor and F4/80 antigen, that it is not required for fetal erythropoiesis, and that its induction on stromal macrophages is delayed until the onset of myeloid and lymphoid development. Sialoadhesin provides a marker to study maturation and functions of macrophages during ontogeny of the lymphohemopoietic system. See generally, Morris et.al., Dev Immunol 2(1):7-17 (1992). PMID: 1521065, UI: 92393348.

The disclosed NOV6 protein of the invention has homology to the murine SN. The murine SN has characteristic properties, as mentioned in the above. The disclosed NOV6

protein of the invention therefore is predicted to have characteristic properties homologous to the murine SN. The expression pattern, map location, and protein similarity information for the invention(s) suggest that NOV6 may function as an SN family member.

The nucleic acids and proteins of the invention are useful in potential therapeutic applications implicated in various diseases and disorders and/or other pathologies and disorders. For example, a cDNA encoding the SN-like protein may be useful in gene therapy, and the SN-like protein may be useful when administered to a subject in need thereof. By way of nonlimiting example, the compositions of the present invention will have efficacy for treatment of patients suffering from from Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation, Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft vesus host, Diabetes, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Xerostomia, Neuroprotection, Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial ephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, Adrenoleukodystrophy, Congenital Adrenal Hyperplasia, Cardiomyopathy, Atherosclerosis, Hypertension, Congenital heart defects, Aortic stenosis, Atrial septal defect (ASD), Atrioventricular (A-V) canal defect, Ductus arteriosus, Pulmonary stenosis, Subaortic stenosis, Ventricular septal defect VSD), valve diseases, Scleroderma, Obesity, Transplantation, Hyperthyroidism, Hypothyroidism, Fertility, Pancreatitis and/or other diseases/pathologies. The novel nucleic acid encoding the SN-like protein, and the SN-like protein of the invention, or fragments thereof, may further be useful in diagnostic applications, wherein the presence or amount of the nucleic acid or the protein are to be assessed. These materials are further useful in the generation of antibodies that bind immunospecifically to the novel substances of the invention for use in therapeutic or diagnostic methods.

Potential therapeutic uses for the invention(s) are, for example but not limited to, the following: (i) Protein therapeutic, (ii) small molecule drug target, (iii) antibody target (therapeutic, diagnostic, drug targeting/cytotoxic antibody), (iv) diagnostic and/or prognostic marker, (v) gene therapy (gene delivery/gene ablation), (vi) research tools, and (vii) tissue

regeneration *in vitro* and *in vivo* (regeneration for all these tissues and cell types composing these tissues and cell types derived from these tissues). The nucleic acids and proteins of the invention are useful in potential therapeutic applications implicated in various diseases and disorders described below and/or other pathologies and disorders.

5 The nucleic acids and proteins of the invention are useful in potential diagnostic and therapeutic applications implicated in various diseases and disorders described above and/or other pathologies. Moreover, the polypeptides can be used as immunogens to produce antibodies specific for the invention, and as vaccines. They can also be used to screen for potential agonist and antagonist compounds. The novel nucleic acid encoding a sialoadhesin-
10 like protein, and the sialoadhesin-like protein of the invention, or fragments thereof, may further be useful in diagnostic applications, wherein the presence or amount of the nucleic acid or the protein are to be assessed.

 These materials are further useful in the generation of antibodies that bind immuno-
specifically to the novel NOV6 substances for use in therapeutic or diagnostic methods. These
15 antibodies may be generated according to methods known in the art, using prediction from hydrophobicity charts, as described in the "Anti-NOVX Antibodies" section below.

NOV7

 NOV7 is a novel protein encoded by a genomic DNA sequence that bears sequence
similarity to Trio. Trio is a phosphoprotein identified in humans (See WO 97/35979) that is
20 suggested to be a central organizer of multiple signaling pathways, to be involved in the activation of oncogenes such as c-fos, and to induce the transformation of cells. Trio has been found to be expressed in several tissues.

 Trio is a complex protein possessing two guanine nucleotide exchange factor domains,
each with adjacent pleckstrin homology and SH3 domains, a protein serine/threonine kinase
25 domain with an adjacent immunoglobulin-like domain and multiple spectrin-like domains. Guanine nucleotide exchange factors, which promote the exchange of GDP for GTP, positively regulate Rho family GTPases and therefore participate in diverse cellular processes, including cell motility and cell growth. There is evidence that expression of fragments of Trio induces haptotactic cell migration and anchorage-independent growth (See Seipel, et al., J Cell Sci 112
30 (Pt 12):1825-34 (1999)).

5

The disclosed NOV7 nucleic acid is shown in Table 7A.

Table 7A. NOV7 Nucleotide Sequence (SEQ ID NO:25)

[illegible]

10

Table 7B. Encoded NOV7 protein sequence (SEQ ID NO:26).

VRKRVFYIYIIKTTPGAEEKSSINHETVMQQLDEAQSQMEELFQERKIKLELFLQLRIFERDAIDVSVPR LAPACLWE
PLASSTAPAPSCCLCPAEVLCPPHPNPLHQEGVWEGERVPGGWNWIIIPGR LGYAQPWTLMLETIEQAARVAGAEHSKR

provided in Table 7C.

Table 7C. Comparison of NOV7 with Trio

AF091395_trio TLQVTYVYIKEGEDLIQQLRDSAISSNKTPHNSINHIETVLQQLDEAQSQMEELFQERK
Ag582_105180778 -----VRKVRFYIYIKITPGAEEKSSINHIETVMQQLDEAQSQMEELFQERK

AF091395_trio IKLELFLHYRIFERDAIDTISDLESWNDELSQGMN--DFDTEDLTIAEQRLQHADKALT
Ag582_105180778 IKLELFLQLRIFERDAIDVSVPR LAPACLWEPLASSTAPAPSCLCPAEVLCPHPHPNPLH

AF091395_trio MNNITFDVIHQSDLLQYVNEVQASGYELLCDRDVDMATRVQDLLFLHEKQQLDLAAE
Ag582_105180778 QEGWEGERVPSGWNWIIPGR LGYAQPWTLMLETIEQARVAGAHSKR-----Alternati

Alternative splice

NOV7 has been analyzed for tissue expression profiles. The quantitative expression of various clones was assessed in normal and tumor tissue samples by real time quantitative PCR (TAQMAN®) as described in Example 1, *infra*.

Figure 1 shows a TaqMan tissue profile result. Two replicates of the same experiment are shown in gray and black bars. It is seen that the alternative splice form is overexpressed in cell lines derived from all major carcinomas groups, melanoma, ovary, lung, kidney, breast, brain. There is no expression, or very low expression, in most normal tissues.

Figure 2 provides replicate TaqMan profiles in a broader range of cancer cells that were derived from surgical specimens. Frequently these are juxtaposed with normal adjacent tissue (NAT) obtained at the same time by the operating surgeon. Figure 2 shows that in colon, lung and kidney carcinomas, the Trio alternative splice form (NOV7) is overexpressed in the tumor compared to the normal adjacent tissue.

The disclosed NOV7 protein (SEQ ID NO:26) has identity with Trio phosphoproteins.

The identity information used for ClustalW analysis is presented in Table 7D.

Table 7D. Identity Information Used for Clustal W Analysis					
Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
gi 13646706 ref XP_003639.3	Triple functional domain (PTPRF interacting) (<i>Homo sapiens</i>)	1201	46/56 (82%)	49/56 (87%)	2e-17
gi 8928460 sp O75962 TRIO_HUMAN; gi 3644048 gb AAC43042.1 (AF091395)	Triple Functional Domain Protein (PTPRF Interacting Protein); Trio isoform (<i>Homo sapien</i>)	3038	44/56 (78%)	48/56 (85%)	1e-16
gi 6005922 ref NP_09049.1 ; gi 3522970 gb AAC34245.1 (U42390)	Triple functional domain (PTPRF interacting) (<i>Homo sapiens</i>)	2861	44/56 (78%)	48/56 (85%)	1e-16
gi 7767545 gb AAF69144.1 AF230644_1 (AF230644)	Kalirin-7c isoform (<i>Rattus norvegicus</i>)	1654	35/48 (72%)	44/48 (90%)	1e-08

gi 13645537 ref XP_003026.2	huntingtin-associated protein interacting protein (<i>Homo sapiens</i>)	1564	35/48 (72%)	44/48 (90%)	1e-08
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This information is presented graphically in the multiple sequence alignment given in Table 7E (with NOV7 being shown on line 1) as a ClustalW analysis comparing NOV7 with related protein sequences.

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Table 7E Information for the ClustalW proteins:

- 1) NOV7 (SEQ ID NO:26)
- 2) gi|136467061 (SEQ ID NO:61)
- 3) gi|89284601 (SEQ ID NO:62)

	10	20	30	40	50	60
NOV7					
gi 136467061	MKAMDVLPILKEKVAYLSGGRDKRGGPILTFPARSNHDIRIQEDLRLISYLACIPSEEV					
gi 89284601	MKAMDVLPILKEKVAYLSGGRDKRGGPILTFPARSNHDIRIQEDLRLISYLACIPSEEV					
	70	80	90	100	110	120
NOV7					
gi 136467061	CKRGFTVIVDMRGSKWDSIKPLLKILQESFPCCIHVALLIKPDNFWQKORTNFGSSKFEF					
gi 89284601	CKRGFTVIVDMRGSKWDSIKPLLKILQESFPCCIHVALLIKPDNFWQKORTNFGSSKFEF					
	130	140	150	160	170	180
NOV7					
gi 136467061	XX					
gi 89284601	ETNMVSLEGLTKVVDPSQLTPEFDGCLYNEHEEWIEIRVAFEDYISNATHMLSRLEELQD					
	190	200	210	220	230	240
NOV7					
gi 136467061	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXDLDLEGQKLLQRIQSSESFPKKNSGS					
gi 89284601	ILAKKELPQDLEGARNMIEEHSQKKKVIKAPIEDLDLEGQKLLQRIQSSESFPKKNSGS					
	250	260	270	280	290	300
NOV7					
gi 136467061	GNADLONLLPKVSTMLDRLHSTROHLHQMWHVRKLLDQCFQLRLFEODA EKMFWDWITHN					
gi 89284601	GNADLONLLPKVSTMLDRLHSTROHLHQMWHVRKLLDQCFQLRLFEODA EKMFWDWITHN					
	310	320	330	340	350	360
NOV7					

NOV7					
gi 13646706	KGLFLNSYTEIGTSHPHAMELQTOHNFAMNCMNVYVNINRIMSVANRLVESGHIYASQOI				
gi 8928460	KGLFLNSYTEIGTSHPHAMELQTOHNFAMNCMNVYVNINRIMSVANRLVESGHIYASQOI				
	370 380 390 400 410 420				
				
NOV7					
gi 13646706	RQIASQLEQEWKAFAAALDERSTLLDMSSIFHQAEKYMSNVDSWCKACGEVDLPSELQD				
gi 8928460	RQIASQLEQEWKAFAAALDERSTLLDMSSIFHQAEKYMSNVDSWCKACGEVDLPSELQD				
	430 440 450 460 470 480				
				
NOV7					
gi 13646706	LEDAlHHHQGIYEHITLAYSEVSQDGKSLDLKQRLTPGSSDSLTAANYSKAVHHVLD				
gi 8928460	LEDAlHHHQGIYEHITLAYSEVSQDGKSLDLKQRLTPGSSDSLTAANYSKAVHHVLD				
	490 500 510 520 530 540				
				
NOV7					
gi 13646706	VIHEVLHHQRIENLWQHRKVRLLHQRLLQCVFOQEVQVLDWIENHGEAFLSKHTGVGKS				
gi 8928460	VIHEVLHHQRIENLWQHRKVRLLHQRLLQCVFOQEVQVLDWIENHGEAFLSKHTGVGKS				
	550 560 570 580 590 600				
				
NOV7					
gi 13646706	LHRARALQKRHEDFEEVAQNTYTNADKLEAAEQLAQTGECDPEEIYQAAHQLEDRIQDF				
gi 8928460	LHRARALQKRHEDFEEVAQNTYTNADKLEAAEQLAQTGECDPEEIYQAAHQLEDRIQDF				
	610 620 630 640 650 660				
				
NOV7					
gi 13646706	VRRVEQRKILLDMSVSFHTHVKEWLTWLEELQKELDDVYAESVEAVODLIKRFQGGQQOT				
gi 8928460	VRRVEQRKILLDMSVSFHTHVKEWLTWLEELQKELDDVYAESVEAVODLIKRFQGGQQOT				
	670 680 690 700 710 720				
				
NOV7					
gi 13646706	TLOVTVNVKEGEDLIQQLRDSAISSNKTPHN--SSINHIETVLQQLDEAQSOMEELFOE				
gi 8928460	TLOVTVNVKEGEDLIQQLRDSAISSNKTPHN--SSINHIETVLQQLDEAQSOMEELFOE				
	730 740 750 760 770 780				
				
NOV7					
gi 13646706	RKIKLELFLQLRIFERDAIDVSVPRAP--				
gi 8928460	RKIKLELFLQLRIFERDAIDVSVPRAP--				
	790 800 810 820 830 840				
				
NOV7					
gi 13646706	ACWEPHASSTAPAPSCLP--AEVLCPPHPN--				
gi 8928460	ACWEPHASSTAPAPSCLP--AEVLCPPHPN--				

gi 13646706	MNNLTFDVIHQGDLLQYVNEVQASGVELLCDRDVDMATRVQDLEFLHEKQOELDAAE
gi 8928460	MNNLTFDVIHQGDLLQYVNEVQASGVELLCDRDVDMATRVQDLEFLHEKQOELDAAE
	850 860 870 880 890 900
NOV7	-----P ¹¹ H ¹² EGVWE--GE-----
gi 13646706	QHRKHLEQCQVLRHLQAEVKQVLGWIRNGESMLNAGLITASSLQEAELQREHEQFQHA
gi 8928460	QHRKHLEQCQVLRHLQAEVKQVLGWIRNGESMLNAGLITASSLQEAELQREHEQFQHA
	910 920 930 940 950 960
NOV7	-----R-----VPGCWN-----
gi 13646706	EKTHQSALQVQKAEAMLQANHYDMDMIRDCAEKVASHWQOLMLKMEDRLKLVNASVAFY
gi 8928460	EKTHQSALQVQKAEAMLQANHYDMDMIRDCAEKVASHWQOLMLKMEDRLKLVNASVAFY
	970 980 990 1000 1010 1020
NOV7	-----
gi 13646706	KTSEQVCSVLESLEQEYKREEDWCGGADKLGPNSETDHVTPMISKHLEQKEAFLKACTLA
gi 8928460	KTSEQVCSVLESLEQEYKREEDWCGGADKLGPNSETDHVTPMISKHLEQKEAFLKACTLA
	1030 1040 1050 1060 1070 1080
NOV7	-----W ¹ I ² P ³ GR ⁴ IG ⁵ Y ⁶ A ⁷ Q ⁸ P-----W ¹ T ² I ³ M ⁴ LE ⁵ T ⁶ E ⁷ Q ⁸ A
gi 13646706	RRNADVFLKYLHRNSVNMPGMVTHIKAPEQOVKNILNELFORENRVLHYWTMRKRRLDOC
gi 8928460	RRNADVFLKYLHRNSVNMPGMVTHIKAPEQOVKNILNELFORENRVLHYWTMRKRRLDOC
	1090 1100 1110 1120 1130 1140
NOV7	ARVAGA ¹ EH ² SK ³ R-----
gi 13646706	QQYVVFERSAKQALEWIHDNGEFYLSHTSTGSSIOHTOELLKEHEEFQITAKOTKERVK
gi 8928460	QQYVVFERSAKQALEWIHDNGEFYLSHTSTGSSIOHTOELLKEHEEFQITAKOTKERVK
	1150 1160 1170 1180 1190 1200
NOV7	-----
gi 13646706	LLIQLADGFCEKGHAHAAEIKKCVTAVDKRYRDFSLRMEKYRTSLEKALGISSDSNKS--
gi 8928460	LLIQLADGFCEKGHAHAAEIKKCVTAVDKRYRDFSLRMEKYRTSLEKALGISSDSNKS
	1210 1220 1230 1240 1250 1260
NOV7	-----
gi 13646706	-----VK ¹ V ² SS-----
gi 8928460	SLQLDIIPASIPGSE ¹ VK ² IRDAAHELNEEKRSARRKEFIMAE ¹ LQTEKAYVRDLRECMDT
	1270 1280 1290 1300 1310 1320
NOV7	-----
gi 13646706	-----

gi 8928460	YLWEMTSGVVEIIPPGIVNKELIIFGNMQEIYEFHNNIFLKELEKYEQLPEDVGHCFTWA
	1330 1340 1350 1360 1370 1380

NOV7	-----
gi 13646706	-----
gi 8928460	DKFQMYVTYCKNKPDPSTQLILEHAGSYFDEIQQRHGLANSISSYLIKPVQRITKYQLLLK
	1390 1400 1410 1420 1430 1440

NOV7	-----
gi 13646706	-----
gi 8928460	ELLTCCEEGKGEIKDGLVMSVPKRAMHLSMLEGFDENIESQGELILQESFQVWDP
	1450 1460 1470 1480 1490 1500

NOV7	-----
gi 13646706	-----
gi 8928460	KTILIRKGRERHLFLFEMSLVFSKEVKDSSGRSKYLYKSKLFTSELGVTEHVEGDPCKFAL
	1510 1520 1530 1540 1550 1560

NOV7	-----
gi 13646706	-----
gi 8928460	WVGRTPTSDNKIVLKASSIENKQDWIKHIREVIQERTIHLKGALKEPIHIPKTAPATRQK
	1570 1580 1590 1600 1610 1620

NOV7	-----
gi 13646706	-----
gi 8928460	GRRDGEDLDSQGDGSSQPDITISIASRTSQNTLSDKLSGGCELTVVIHDFACNSNELTI
	1630 1640 1650 1660 1670 1680

NOV7	-----
gi 13646706	-----
gi 8928460	RRGQTVEVLERPHDKPDWCLVRTTDRSPAAEGLVPCGSLCIAHSRSSMEMEGIFNHKDSL
	1690 1700 1710 1720 1730 1740

NOV7	-----
gi 13646706	-----
gi 8928460	SVSSNDASPPASVASLQPHMIGAQSSPGPKRPGNTLRKWLTSVPRRLSSGKADGHVKKLA
	1750 1760 1770 1780 1790 1800

NOV7	-----
gi 13646706	-----
gi 8928460	HKKHKSREVRKSADAGSQKSDSDSAATPQDETVEERGRNEGLSSGTLKSSSSGMQSCGE

	1810	1820	1830	1840	1850	1860
					
NOV7	-----					
gi 13646706	-----					
gi 8928460	EEGEEGADAVPLPPMAIQQHSLLPDSQDDKASSRLVLRPTSSETPSAAELVSAIEELV					
	1870	1880	1890	1900	1910	1920
					
NOV7	-----					
gi 13646706	-----					
gi 8928460	KSKMALEDPRSSLLVDQGDSSSPSFNPSPDNSLLSSSSPIDEMEERKSSSLKRRHYVLQEL					
	1930	1940	1950	1960	1970	1980
					
NOV7	-----					
gi 13646706	-----					
gi 8928460	VETERDYVRDLGYVVEGYMALMKEDGVPDDMKGKDKIVFGNIHQIYDWHRDFFLGELEKC					
	1990	2000	2010	2020	2030	2040
					
NOV7	-----					
gi 13646706	-----					
gi 8928460	LEDPEKLGSLFVKHERRLHMYIAYCQNKPKSEHIVSEYIDTFFEDLKQRLGHRQLTDL					
	2050	2060	2070	2080	2090	2100
					
NOV7	-----					
gi 13646706	-----					
gi 8928460	IKPVQRIMKYQLLLKDFLKYSKKASLDTSELERAVEVMCIVPRRCNDMMNVGRLQGFDGK					
	2110	2120	2130	2140	2150	2160
					
NOV7	-----					
gi 13646706	-----					
gi 8928460	IVAQGKLLQDTFLVTDQDAGLLPRCRERRIFLFEQIVIFSEPLDKKGFSGMPGFLFKNS					
	2170	2180	2190	2200	2210	2220
					
NOV7	-----					
gi 13646706	-----					
gi 8928460	IKVSCLCLEENVENDPCKFALTSTRTGDVVETFILHSSSPSVRQTWIHEINQILENQRNFL					
	2230	2240	2250	2260	2270	2280
					
NOV7	-----					
gi 13646706	-----					
gi 8928460	NALTSPIEYQRNHSGGGGGGGGGGGGGGGGGGGGGGGGGAPSGGSGHSGGPSSCGGAPSTSRSR					

	2290	2300	2310	2320	2330	2340
					
NOV7	-----					
gi 13646706	-----					
gi 8928460	PSRIPQPVRRHPPVLVSSAASSQAEADKMSGTSTPGPSLPPPGAAPAEAGPSAPSRPPGA					
	2350	2360	2370	2380	2390	2400
					
NOV7	-----					
gi 13646706	-----					
gi 8928460	DAEGSERAEPKPKMKVLESPRGAANASGSSPDAPAKDARASLGTLPLGKPRAGAASPL					
	2410	2420	2430	2440	2450	2460
					
NOV7	-----					
gi 13646706	-----					
gi 8928460	NSPLSSAVPSLGKEFPFPSSPLQKGSFWSSIPASPASRPGSFTFPGDSDSLQRQTPRHA					
	2470	2480	2490	2500	2510	2520
					
NOV7	-----					
gi 13646706	-----					
gi 8928460	APGKDTDRMSTCSSASEQSVQSTQSNSESSSSSNISTMLVTHDYTAVKEDEINVYQGEV					
	2530	2540	2550	2560	2570	2580
					
NOV7	-----					
gi 13646706	-----					
gi 8928460	VQILASNQQNMFLVFRAATDQCPAAEGWIPGFVLGHTSAVIVENPDGTLKKSTSWHTALR					
	2590	2600	2610	2620	2630	2640
					
NOV7	-----					
gi 13646706	-----					
gi 8928460	LRKKSEKKDKDGKREGKLENGYRKSREGLSNKVSVKLLNPNIYDVPPEFVIPLSEVTCE					
	2650	2660	2670	2680	2690	2700
					
NOV7	-----					
gi 13646706	-----					
gi 8928460	TGETVVLRRCRVCGRPKASITWKGPEHNTLNNDGHYSISYSDLGEATLKIVGVTTEDDGIY					
	2710	2720	2730	2740	2750	2760
					
NOV7	-----					
gi 13646706	-----					
gi 8928460	TCIAVNDMGSASSASLRVLGPGMDGIMVTWKDNFDSFYSEVAELGRGRFSVVKKCDQKG					
	2770	2780	2790	2800	2810	2820

[illegible]

5

Table 7F. Patp alignments of NOV7

Table 7F. Patp alignments of NOV7			
Sequences producing High-scoring Segment Pairs:	Reading Frame	High Score	Smallest Sum Prob. P(N)
Patp:AAW27227 Human TRIO phosphoprotein, 2861 aa	+2	216	9.8e-13

For example, a BLAST against patp: AAW27227, a 2861 amino acid TRIO phosphoprotein (WO97/35979), produced good identity, $E = 9.8e-13$).

The similarity information for the NOV7 protein and nucleic acid disclosed herein suggest that NOV7 may have important structural and/or physiological functions characteristic of Trio. Therefore, the nucleic acids and proteins of the invention are useful in potential diagnostic and therapeutic applications and as a research tool. These include serving as a specific or selective nucleic acid or protein diagnostic and/or prognostic marker, wherein the presence or amount of the nucleic acid or the protein are to be assessed, as well as potential therapeutic applications such as the following: (i) a protein therapeutic, (ii) a small molecule drug target, (iii) an antibody target (therapeutic, diagnostic, drug targeting/cytotoxic antibody), (iv) a nucleic acid useful in gene therapy (gene delivery/gene ablation), and (v) a composition promoting tissue regeneration *in vitro* and *in vivo* (vi) biological defense weapon. The novel nucleic acid encoding NOV7, and the disclosed NOV7 protein, or fragments thereof, may further be useful in diagnostic applications, wherein the presence or amount of the nucleic acid or the protein are to be assessed.

The disclosed NOV7 polypeptides can be used as immunogens to produce vaccines. The novel nucleic acid encoding NOV-like protein, and the NOV-like protein of the invention, or fragments thereof, may further be useful in diagnostic applications, wherein the presence or amount of the nucleic acid or the protein are to be assessed. These materials are further useful in the generation of antibodies that bind immunospecifically to the novel substances of the invention for use in therapeutic or diagnostic methods. For example the disclosed NOV7 protein has multiple hydrophilic regions, each of which can be used as an immunogen. These novel proteins can also be used to develop assay system for functional analysis. These antibodies may be generated according to methods known in the art, using prediction from hydrophobicity charts, as described in the "Anti-NOVX Antibodies" section below.

NOV8

The present invention discloses a novel protein encoded by a cDNA and/or genomic DNA and proteins similar to it, namely, proteins bearing sequence similarity to Stra6

NOV8a

This invention describes the following novel Stra6-like proteins and nucleic acids encoding them: 3277789_EXT (NOV8a). These sequences were initially identified by searching CuraGen's Human SeqCalling database for DNA sequences, which translate into proteins with similarity to Stra6-Like Proteins. SeqCalling is a differential expression and

sequencing procedure that normalizes mRNA species in a sample, and is disclosed in U.S. Ser. No. 09/417,386, filed Oct. 13, 1999, incorporated herein by reference in its entirety. SeqCalling assembly 3277789 was identified as having suitable similarity. NOV8a was analyzed further to identify any open reading frames encoding novel full length proteins as well as novel splice forms of these genes. The SeqCalling assembly was extended using one or more sequences taken from additional SeqCalling assemblies, publicly available EST sequences and public genomic sequences. Public ESTs and additional CuraGen SeqCalling assemblies were identified by the CuraTools™ program SeqExtend. Such fragments were included in the DNA sequence extension for SeqCalling assembly 3277789 only when the extent of identity in the putative overlap region was high. The extent of identity may be, for example, about 90% or higher, preferably about 95% or higher, and even more preferably close to or equal to 100%. These inclusions, if used, are described below.

Genomic clone (acc:AC023545 HTG Homo sapiens chromosome 15 clone RP11-665J16 map 15, WORKING DRAFT SEQUENCE, 28 unordered pieces - *Homo sapiens*) was analyzed by Genscan and Grail to identify exons and putative coding sequences. This clone was also analyzed by TblastN, BlastX and other programs to identify genomic regions translating to proteins with similarity to the original protein or protein family of interest. It was identified as having regions with 100% identity to the SeqCalling assembly 3277789.

The results of these analyses were integrated and manually corrected for apparent inconsistencies that may have arisen, for example, from miscalled bases in the original fragments used. The sequences obtained encode the full-length proteins disclosed herein. When necessary, the process to identify and analyze cDNAs, ESTs and genomic clones was reiterated to derive the full-length sequence.

The disclosed NOV8a nucleic acid of 1962 nucleotides (also referred to as 3277789_EXT) is shown in Table 8A. An open reading begins with an ATG initiation codon at nucleotides 1-3 and ends with a TGA codon at nucleotides 1960-1962.

Table 8A. NOV8a Nucleotide Sequence (SEQ ID NO:27)

ATGTCGTCCCAGCCAGCAGGGAACCAGACCTCCCCGGGGCCACAGAGGACTACTCCTATGGCAGCTGGT
ACATCGATGAGCCCCAGGGGGCGAGGAGCTCCAGCCAGAGGGGAAGTGCCCTCCTGCCACACCAGCAT
ACCACCCGGCCTGTACCACGCCTGCCTGGCCTCGCTGTCAATCCTTGTGCTGCTGCTCCTGGCCATGCTG
GTGAGGCGCCGCCAGCTCTGGCCTGACTGTGTGCGTGGCAGGCCCGGCCTGCCAGCCCTGTGGATTTCT
TGGCTGGGGACAGGCCCGGGCAGTGCCTGCTGCTGTTTTTCATGGTCCTCCTGAGCTCCCTGTGTTTGCT
GCTCCCCGACGAGGACGCATTGCCCTTCCTGACTCTCGCCTCAGCACCCAGCGGGGCTGGAAGATACTG
GGACTGTTCTATTATGCTGCCCTCTACTACCTCTGGCTGCCTGTGCCACGGCTGGCCACACAGCTGCAC
ACCTGCTCGGCAGCACGCTGCTCCTGGGCCACCTTGGGGTCCAGGTCTGGCAGAGGGCAGAGTGTCCCCA

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GGTGCCCAAGATCTACAAGTACTACTCCCTGCTGGCCTCCCTGCCTCTCCTGCTGGGCTCGGATTCCCTG
AGCCTTTGGTACCCTGTGCAGCTGGTGAGAAGCTTCAGCCGTAGGACAGGAGCAGGCTCCCAGGGGCTGC
AGAGCAGCTACTCTGAGGAATATCTGAGGAACCTCCTTTGCAGGAAGAAGCTGGGAAGCTGCAGCTACCA
CACCTCCAAGCATGGCTTCTGTCTGGGCCCGCGTCTGCTTGAGACACTGCATCTACTACTCCACAGCCA
GGATTCCATCTCCCGCTGAAGCTGGTGCTTTTCAGCTACACTGACAGGGACGGCCATTACCAGGTAGCCC
TGCTGCTGCTGGTGGGCGTGGTACCCACTATCCAGAAGGTGAGGGCAGGGGTACCACGGATGTCTCCTA
CCTGCTGGCCGGCTTTGGAATCGTGCTCTCCGAGGACAAGCAGGAGGTGGTGGAGCTGGTGAAGCACCAT
CTGTGGGCTCTGGAAGTGTGCTACATCTCAGCCTTGGTCTTGTCTGCTTACTCACCTTCTGGTCTCTGA
TGCGCTCACTGGTGACACACAGGACCAACCTTCGAGCTCTGCACCGAGGAGCTGCCCTGGACTTGAGTCC
CTTGTCATCGGAGTCCCCATCCCTCCCGCCAAGCCATATTCTGTTGGATGAGCTTCAGTGCCTACCAGACA
GCCTTTATCTGCCTTGGTCTCCTGGTGCAGCAGATCATCTTCTTCTGGAACACGGCCCTGGCCTTCC
TGGTGCTCATGCCTGTGTCTCCATGGCAGGAACCTCCTGCTCTTCCGTTCCCTGGAGTCCCTCATGGCCCTG
GCTTGTGATCCTGCAGAACATGGCAGCCCATTTGGGTCTTCTGGAGACTCATGATGGACACCCACAGCTG
ACCAACCGGCGAGTGCTCTATGCAGCCACCTTTCTTCTTCCCCCTCAATGTGCTGGTGGGTGCCATGG
TGGCCACCTGGCGAGTGCTCTCTGCCCCTCTACAACGCCATCCACCTTGGCCAGATGGACCTCAGCCT
GCTGCCACCGAGAGCGCCACTCTCGACCCAGGCTACTACAGTACCGAACTTCTTGAAGATTGAAGTC
AGCCAGTCGCATCCAGCCATGACAGCCTTCTGCTCCCTGCTCCTGCAAGCGCAGAGCCTCCTACCCAGGA
CCATGGCAGCCCCCAGGACAGCCTCAGACCAGGGGAGGAAGACGAAGGTATGCAGCTGCTACAGACAAA
GGACTCCATGGCCAAGGGAGCTAGGCCCGGGGCCAGCCGCGGCAGGGCTCGCTGGGGTCTGGCCTACACG
CTGCTGCACAACCCAACCTGCAGGTCTTCCGCAAGACGGCCCTGTGGGTGCCAATGGTGCCAGCCCT
GA

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The NOV8a protein encoded by SEQ ID NO:27 has 653 amino acid residues, and is presented using the one-letter code in Table 8B (SEQ ID NO:28). The SignalP, Psort and/or Hydropathy profile for NOV8 predict that NOV8 has a signal peptide and is likely to be localized within the plasma membrane with a certainty of 0.6000. It is also likely localized at the Golgi body (certainty = 0.4000); endoplasmic reticulum (membrane) (certainty = 0.3000); and microbody (peroxisome) (certainty = 0.3000). The disclosed NOV8a protein is predicted to have a signal peptide that is likely cleaved between positions 8 and 9 (*i.e.*, at the slash in the sequence AGN-QT).

Table 8B. Encoded NOV8a protein sequence (SEQ ID NO:28).

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MSSQPAGNQTSFGATEDYSYGSWYIDEPQGGEELOPEGEVPSCHTSIPPGLYHACLASLSILVLLLLAML
VRRRLWPDVCVRGRPLSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDEDALPFLTASAPSGAWKIL
GLFYAALYYPLAACATAGHTAAHLLGSTLSWAHLGVQVWQRAECPQVPKIYKYYSLLASLPLLLGLGFL
SLWYPVQLVRSFRRRTGAGSQGLQSSYSEEYLRNLLCRKKLGSCSYHTSKHGFLSWARVCLRHCITYPQP
GFHLPLKLVLSTLTGTATYQVALLLLVGVPVTIQKVRAGVTTDVSYLLAGFGIVLSEDKQEVVELVKHH
LWALEVCYISALVLSCLLTFVLVLMRSLVTHRTNLRALHRGAALDLSPLHRSPHPSRQAIFCWMSFSAYQT
AFICLGLLVQIIFFLGTALAFVLMPVLHGRNLLFRSLESSWPVLVILQNMAAHWFLETHDGHFQL
TNRRVLYAATFLLFPLNVLVGAMVATWRVLLSALYNAILHGMQLSLLPPRAATLDPGYTYRNFLEKIEV
SQSHPMATAFCSLLQAQSLPRTMAAPQDSLPGEEDEGMQLLQTKDSMAKGARPGASRGARWGLAYT
LLHNPTLQVFRKTALLGANGAQF

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The disclosed Stra6-like protein (NOV8a) maps to chromosome 15. Additionally, the disclosed NOV8a protein is expressed in at least the following tissues: testis, bone, muscle, and blood-organ barriers. The protein disclosed herein is similar to the “Stra6-Like Protein Family”, some members of which end up localized at the cell surface where they exhibit

activity. Therefore, it is likely that this novel Stra6-Like Protein is available at the appropriate sub-cellular localization and hence accessible for the therapeutic uses described herein.

NOV8b

5 In the present invention, the target sequence identified previously, Accession Number 3277789_Ext or CG52276-01 (NOV8a), was subjected to the exon linking process to confirm the sequence. PCR primers were designed by starting at the most upstream sequence available, for the forward primer, and at the most downstream sequence available for the reverse primer. In each case, the sequence was examined, walking inward from the respective termini toward
10 the coding sequence, until a suitable sequence that is either unique or highly selective was encountered, or, in the case of the reverse primer, until the stop codon was reached. Such primers were designed based on *in silico* predictions for the full length cDNA, part (one or more exons) of the DNA or protein sequence of the target sequence, or by translated homology of the predicted exons to closely related human sequences sequences from other species. These
15 primers were then employed in PCR amplification based on the following pool of human cDNAs: adrenal gland, bone marrow, brain - amygdala, brain - cerebellum, brain - hippocampus, brain - substantia nigra, brain - thalamus, brain -whole, fetal brain, fetal kidney, fetal liver, fetal lung, heart, kidney, lymphoma - Raji, mammary gland, pancreas, pituitary gland, placenta, prostate, salivary gland, skeletal muscle, small intestine, spinal cord, spleen,
20 stomach, testis, thyroid, trachea, uterus. Usually the resulting amplicons were gel purified, cloned and sequenced to high redundancy. The resulting sequences from all clones were assembled with themselves, with other fragments in CuraGen Corporation's database and with public ESTs. Fragments and ESTs were included as components for an assembly when the extent of their identity with another component of the assembly was at least 95% over 50 bp. In
25 addition, sequence traces were evaluated manually and edited for corrections if appropriate. These procedures provide the sequence reported below, which is designated Accession Number CG52276-03 (NOV8b). NOV8b is a splice variant form and differs from the previously identified sequence (NOV8a) in having 9 additional internal amino acids and one amino acid change at position 59 S->P.

30 The sequence of the invention was derived by laboratory cloning of cDNA fragments covering the full length and/or part of the DNA sequence of the invention, and/or by *in silico*

prediction of the full length and/or part of the DNA sequence of the invention from public human sequence databases.

The laboratory cloning was performed using one or more of the methods summarized below:

5 *SeqCalling™ Technology*: cDNA was derived from various human samples representing multiple tissue types, normal and diseased states, physiological states, and developmental states from different donors. Samples were obtained as whole tissue, cell lines, primary cells or tissue cultured primary cells and cell lines. Cells and cell lines may have been treated with biological or chemical agents that regulate gene expression for example, growth
10 factors, chemokines, steroids. The cDNA thus derived was then sequenced using CuraGen's proprietary SeqCalling technology. Sequence traces were evaluated manually and edited for corrections if appropriate. cDNA sequences from all samples were assembled with themselves and with public ESTs using bioinformatics programs to generate CuraGen's human SeqCalling database of SeqCalling assemblies. Each assembly contains one or more overlapping cDNA
15 sequences derived from one or more human samples. Fragments and ESTs were included as components for an assembly when the extent of identity with another component of the assembly was at least 95% over 50 bp. Each assembly can represent a gene and/or its variants such as splice forms and/or single nucleotide polymorphisms (SNPs) and their combinations.

Exon Linking: The cDNA coding for the sequence was cloned by polymerase chain
20 reaction (PCR) using the following primers: GGTCAAAGGAGAAGGGCCAGAGAAT (SEQ ID NO:63) and TTTTCTCAGGACCAAGTTTATTGCAGG (SEQ ID NO:64) on the following pool of human cDNAs: Pool 1 - Adrenal gland, bone marrow, brain - amygdala, brain - cerebellum, brain - hippocampus, brain - substantia nigra, brain - thalamus, brain - whole, fetal brain, fetal kidney, fetal liver, fetal lung, heart, kidney, lymphoma - Raji, mammary gland,
25 pancreas, pituitary gland, placenta, prostate, salivary gland, skeletal muscle, small intestine, spinal cord, spleen, stomach, testis, thyroid, trachea, uterus.

 Primers were designed based on *in silico* predictions for the full length or part (one or more exons) of the DNA/protein sequence of the invention or by translated homology of the predicted exons to closely related human sequences or to sequences from other species. Usually
30 multiple clones were sequenced to derive the sequence which was then assembled similar to the SeqCalling process. In addition, sequence traces were evaluated manually and edited for corrections if appropriate.

Variant sequences are also included in this application. A variant sequence can include a single nucleotide polymorphism (SNP). A SNP can, in some instances, be referred to as a "cSNP" to denote that the nucleotide sequence containing the SNP originates as a cDNA. A SNP can arise in several ways. For example, a SNP may be due to a substitution of one nucleotide for another at the polymorphic site. Such a substitution can be either a transition or a transversion. A SNP can also arise from a deletion of a nucleotide or an insertion of a nucleotide, relative to a reference allele. In this case, the polymorphic site is a site at which one allele bears a gap with respect to a particular nucleotide in another allele. SNPs occurring within genes may result in an alteration of the amino acid encoded by the gene at the position of the SNP. Intragenic SNPs may also be silent, however, in the case that a codon including a SNP encodes the same amino acid as a result of the redundancy of the genetic code. SNPs occurring outside the region of a gene, or in an intron within a gene, do not result in changes in any amino acid sequence of a protein but may result in altered regulation of the expression pattern for example, alteration in temporal expression, physiological response regulation, cell type expression regulation, intensity of expression, stability of transcribed message.

The DNA sequence and protein sequence for a novel Retinoic Acid-Responsive Protein-like gene or one of its splice forms was obtained solely by exon linking and is reported here as NOV8b.

The disclosed NOV8b nucleic acid of 2012 bp (SEQ ID NO:29) is shown in Table 8C. An open reading frame was identified beginning at nucleotides 24-26 and ending at nucleotides 2010-2012. The start (ATG) and stop (TGA) codons of the open reading frame are highlighted in bold type. Putative untranslated regions, if any, are underlined.

Table 8C. NOV8b Nucleotide Sequence (SEQ ID NO:29)

GGTCAAAGGAGAAGGGCCAGAGA**ATG**TCGTCCCAGCCAGCAGGGAACCAGACCTCCCCCG
 GGGCCACAGAGGACTACTCCTATGGCAGCTGGTACATCGATGAGCCCCAGGGGGCGAGG
 AGTCCAGCCAGAGGGGAAGTGCCCTCCTGCCACACCAGCATACCACCCGGCCTGTACC
 ACGCTGCCTGGCCCCACTGTCAATCCTTGTGCTGCTGCTCCTGGCCATGCTGGTGAGGC
 GCCGCCAGCTCTGGCCTGACTGTGTGCGTGGCAGGCCCGGCCTGCCAGCCCTGTGGATT
 TCTTGCTGGGGACAGGCCCCGGGCAGTGCCTGCTGCTGTTTTTCATGGTCCTCCTGAGCT
 CCCTGTGTTTGCTGCTCCCCGACGAGGACGCATTGCCCTTCCTGACTCTCGCCTCAGCAC
 CCAGCCAAGATGGGAAACTGAGGCTCCAAGAGGGGCCTGGAAGATACTGGGACTGTTCT
 ATTATGCTGCCCTCTACTACCCTCTGGCTGCCTGTGCCACGGCTGGCCACACAGCTGCAC
 ACCTGCTCGGCAGCACGCTGTCCTGGGCCACCTTGGGGTCCAGGTCTGGCAGAGGGCAG
 AGTGTCCTCCAGGTGCCAAGATCTACAAGTACTACTCCCTGCTGGCCTCCCTGCCTCTCC
 TGCTGGGCCTCGGATTCTGAGCCTTTGGTACCCTGTGCAGCTGGTGAGAAGCTTCAGCC
 GTAGGACAGGAGCAGGCTCCCAGGGGCTGCAGAGCAGCTACTCTGAGGAATATCTGAGGA
 ACCTCCTTTGCAGGAAGAAGCTGGGAAGCTGCAGCTACCACACCTCCAAGCATGGCTTCC
 TGCTCTGGGCCCCGCTGCTGTGAGACACTGCATCTACACTCCACAGCCAGGATTCCATC
 TCCCGCTGAAGCTGGTGCTTTCAGCTACACTGACAGGGACGGCCATTTACCAGGTAGCCC
 TGCTGCTGCTGGTGGGCGTGGTACCCACTATCCAGAAGGTGAGGGCAGGGGTACCCACGG
 ATGCTCCTACCTGCTGGCCGGCTTTGGAATCGTGCTCTCCGAGGACAAGCAGGAGGTGG
 TGGAGCTGGTGAAGCACCATCTGTGGGCTCTGGAAGTGTGCTACATCTCAGCCTTGGTCT
 TGTCCTGCTTACTCACCTTCCTGGTCCTGATGCGCTCACTGGTGACACACAGGACCAACC
 TTCGAGCTCTGCACCGAGGAGCTGCCCTGGACTTGAGTCCCTTGCATCGGAGTCCCCATC
 CCTCCCGCCAAGCCATATTCTGTTGGATGAGCTTCAGTGCCTACCAGACAGCCTTTATCT
 GCCTTGGTCTCCTGGTGCAGCAGATCATCTTCTTCTGGAACACGGCCCTGGCCTTCC
 TGGTGCTCATGCCTGTGCTCCATGGCAGGAACCTCCTGCTCTCCGTTCCCTGGAGTCCT
 CATGGCCCTGGCTTGTGATCCTGCAGAACATGGCAGCCCATTTGGGTCTTCTGGAGACTC
 ATGATGGACACCCACAGCTGACCAACCGCGAGTGCTCTATGCAGCCACCTTTCTTCTCT
 TCCCCCTCAATGTGCTGGTGGGTGCCATGGTGGCCACCTGGCGAGTGCTCCTCTCTGCCC
 TCTACAACGCCATCCACCTTGGCCAGATGGACCTCAGCCTGCTGCCACCGAGAGCCGCCA
 CTCTCGACCCAGGCTACTACACGTACCGAACTTCTTGAAGATTGAAGTCAGCCAGTCGC
 ATCCAGCCATGACAGCCTTCTGCTCCCTGCTCCTGCAAGCGCAGAGCCTCCTACCCAGGA
 CCATGGCAGCCCCCAGGACAGCCTCAGACCAGGGGAGGAAGACGAAGGTATGCAGCTGC
 TACAGACAAAGGACTCCATGGCCAAGGGAGCTAGGCCCGGGGCCAGCCGCGGCAGGGCTC
 GCTGGGGTCTGGCCTACACGCTGCTGCACAACCCAACCTGCAGGTCTTCCGCAAGACGG
 CCCTGTTGGGTGCCAATGGTGCCAGCCCTGA

The NOV8b protein encoded by SEQ ID NO:29 has 662 amino acid residues, and is
 presented using the one-letter code in Table 8D (SEQ ID NO:30). The SignalP, Psort and
 Hydropathy profile for the Retinoic Acid-Responsive Protein-like protein predict that this
 5 sequence has a signal peptide and is likely to be localized at the plasma membrane with a
 certainty of 0.6000. NOV8b is also likely localized to the Golgi body (certainty = 0.4000);

endoplasmic reticulum (membrane) (certainty = 0.3000); and microbody (peroxisome) (certainty = 0.3000). The first 8 amino acids are more likely to be cleaved as a signal peptide based on the SignalP result (*i.e.*, between the slash in the sequence AGN-QT).

Table 8D. Encoded NOV8b protein sequence (SEQ ID NO:30).

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MSSQPAGNQTSFGATEDYSYGSWYIDEPQGGEELQPEGEVPSCHTSIPPGLYHACLAPLS
ILVLLLLLAMLVRRRQLWPCVGRGPLSPVDFLAGDRPRAPVAAVFMVLLSSLCLLLPD
EDALPFLTLASAPSQDGKTEAPRGAWKILGLFYAALYYPLAACATAGHTAAHLLGSTLS
WAHLGVQVWQRAECPQVPKIYKYSSLASPLLLGLGFLSLWYPVQLVRSFSRRTGAGSQ
GLQSSYSEEYLRNLLCRKKLGSCSYHTSKHGFLSWARVCLRHCIYTPQPGFHLPLKLVL
ATLTGTAIYQVALLLVGVPTIQKVRAGVTTDVSYLLAGFGIVLSEDKQEVVELVKHHL
WALEVCYISALVLSCLLTFVLMLRSLVTHRTNLRALHRGAALDLSPLHRSPHPSRQAIFC
WMSFSAYQTAFICLGLLVQQIIFFLGTTALAFVLMPVLHGRNLLFRSLESSWPWLVL
QNMAAHWVFLETHDGHPQLTNRRLVYAATFLLFPLNVLVGAMVATWRVLLSALYNAIHLG
QMDLSLLPPRAATLDPGYTYRNFLKIEVSQSHPAMTAFCSLLQAQSLLPRTMAAPQDS
LRPGEEDGMQLLQTKDSMAKGARPGASRGRRARWGLAYTLLHNPTLQVFRKTALLGANGA
QP

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The disclosed NOV8b disclosed in this invention is expressed in at least the following tissues: Brain, Cervix, Heart, Kidney, Lymph node, Lymphoid tissue, Ovary, Pituitary Gland, Placenta, Retina, Temporal Lobe, Thyroid, Uterus, Whole Organism. This information was derived by determining the tissue sources of the sequences that were included in the invention including but not limited to SeqCalling sources, Public EST sources, Literature sources, and/or RACE sources.

NOV8c

The sequence of Acc. No. CG52276-04 (NOV8c) was derived by laboratory cloning of cDNA fragments, by *in silico* prediction of the sequence. cDNA fragments covering either the full length of the DNA sequence, or part of the sequence, or both, were cloned. *In silico* prediction was based on sequences available in Curagen's proprietary sequence databases or in the public human sequence databases, and provided either the full-length DNA sequence, or some portion thereof.

Exon Linking: The cDNA coding for the CG52276-04 sequence was cloned by the polymerase chain reaction (PCR) using the primers: 5' GTCAAAGGAGAAGGGCCAGAGAAT 3' (SEQ ID NO:65) and 5'

TTTTCTCAGGACCAAGTTTATTGCAGG 3' (SEQ ID NO:66). Primers were designed based on *in silico* predictions of the full length or some portion (one or more exons) of the cDNA/protein sequence of the invention. These primers were used to amplify a cDNA from a pool containing expressed human sequences derived from the following tissues: adrenal gland, bone marrow, brain - amygdala, brain - cerebellum, brain - hippocampus, brain - substantia nigra, brain - thalamus, brain - whole, fetal brain, fetal kidney, fetal liver, fetal lung, heart, kidney, lymphoma - Raji, mammary gland, pancreas, pituitary gland, placenta, prostate, salivary gland, skeletal muscle, small intestine, spinal cord, spleen, stomach, testis, thyroid, trachea and uterus.

Multiple clones were sequenced and these fragments were assembled together, sometimes including public human sequences, using bioinformatic programs to produce a consensus sequence for each assembly. Each assembly is included in CuraGen Corporation's database. Sequences were included as components for assembly when the extent of identity with another component was at least 95% over 50 bp. Each assembly represents a gene or portion thereof and includes information on variants, such as splice forms single nucleotide polymorphisms (SNPs), insertions, deletions and other sequence variations.

Physical clone: The PCR product derived by exon linking, covering the entire open reading frame, was cloned into the pCR2.1 vector from Invitrogen to provide clone 90816::3277789.698482.C4.

Variant sequences are also included in this application. A variant sequence can include a single nucleotide polymorphism (SNP). A SNP can, in some instances, be referred to as a "cSNP" to denote that the nucleotide sequence containing the SNP originates as a cDNA. A SNP can arise in several ways. For example, a SNP may be due to a substitution of one nucleotide for another at the polymorphic site. Such a substitution can be either a transition or a transversion. A SNP can also arise from a deletion of a nucleotide or an insertion of a nucleotide, relative to a reference allele. In this case, the polymorphic site is a site at which one allele bears a gap with respect to a particular nucleotide in another allele. SNPs occurring within genes may result in an alteration of the amino acid encoded by the gene at the position of the SNP. Intragenic SNPs may also be silent, when a codon including a SNP encodes the same amino acid as a result of the redundancy of the genetic code. SNPs occurring outside the region of a gene, or in an intron within a gene, do not result in changes in any amino acid sequence of a protein but may result in altered regulation of the expression pattern. Examples include

alteration in temporal expression, physiological response regulation, cell type expression regulation, intensity of expression, and stability of transcribed message.

The DNA sequence and protein sequence for a novel Retinoic Acid Responsive-like gene were obtained by exon linking and are reported here as NOV8c (CuraGen Acc. No.

CG52276-04).

The disclosed NOV8c nucleic acid of 2620 bp (SEQ ID NO:31) is shown in Table 8E. An open reading frame was identified beginning at nucleotides 24-26 and ending at nucleotides 2025-2027. The start (ATG) and stop (TGA) codons of the open reading frame are highlighted in bold type. Putative untranslated regions, if any, are underlined.

Table 8E. NOV8c Nucleotide Sequence (SEQ ID NO:31)

GGTCAAAGGAGAAGGGCCAGAGA**ATG**TCGTCCAGCCAGCAGGGAAACCAGACCTCCCCCG
GGGCCACAGAGGACTACTCCTATGGCAGCTGGTACATCGATGAGCCCCAGGGGGGCGAGG
AGCTCCAGCCAGAGGGGAAGTGCCCTCCTGCCACACCAGCATACCACCGGCCCTGTACC
ACGCCTGCCTGGCCTCGCTGTCAATCCTTGTGCTGCTGCTCCTGGCCATGCTGGTGAGGC
GCCGCCAGCTCTGGCCTGACTGTGTGCGTGGCAGGCCCGGCCCTGCCAGCCCTGTGGATT
TCTTGCTGGGGACAGGCCCGGGCAGTGCCTGCTGCTGTTTTCATGATCCTCCTGAGCT
CCCTGTGTTTGTGCTGCTCCCCGACGAGGACGCATTGCCCTTCCTGACTCTCGCCTCAGCAC
CCAGCCAAGATGGGAAAAGTGAAGCTCCAAGAGGGGCTGGAAGATACTGGGACTGTTCT
ATTATGCTGCCCTCTACTACCTCTGGCTGCCTGTGCCACGGCTGGCCACACAGCTGCAC
ACCTGCTCGGCAGCACGCTGTCTGGGCCACCTTGGGGTCCAGGTCTGGCAGAGGGCAG
AGTGTCCCCAGGTGCCCCAAGATCTACAAGTACTACTCCCTGCTGCCCTCCCTGCCTCTCC
TGCTGGGCTCGGATTCTTGAGCCTTTGGTACCCTGTGCAGCTGGTGAGAAGCTTCAGCC
GTAGGACAGGAGCAGGCTCCAAGGGGCTGCAGAGCAGCTACTCTGAGGAATATCTGAGGA
ACCTCCTTTGCAGGAAGAAGCTGGGAAGCAGTACCACACCTCCAAGCATGGCTTCCTGT
CCTGGGCCCGCGTCTGCTTGAGACACTGCATCTACACTCCACAGCCAGGATTCCATCTCC
CGCTGAAGCTGGTGCTTTTCACTACACTGACAGGGACGGCCATTACCAGGTGGCCCTGC
TGCTGCTGGTGGGCGTGGTACCCACTATCCAGAAGGTGAGGGCAGGGGTACCCACGGATG
TCTCTACCTGCTGGCCGGCTTTGGAATCGTGCTCTCCGAGGACAAGCAGGAGGTGGTGG
AGCTGGTGAAGCACCATCTGTGGGCTCTGGAAGTGTGCTACATCTCAGCCTTGGTCTTGT
CCTGCTTACTCACCTTCCTGGTCTGATGCGCTCACTGGTGACACACAGGACCAACCTTC
GAGCTCTGCACCGAGGAGCTGCCCTGGACTTGAGTCCCTTGCACTCGGAGTCCCCATCCCT
CCCCCAAGCCATATCTGTTGGATGAGCTTCAGTGCCTACCAGACAGCCTTTATCTGCC
TTGGGCTCCTGGTGCAGCAGATCATCTTCTTCTTGGGAACCACGGCCCTGGCCTTCCTGG
TGCTCATGCCTGTGCTCCATGGCAGGAACCTCCTGCTCTTCCGTTCCTGGAGTCCTCGT
GGCCCTTCTGGCTGACTTTGGCCCTGGCTGTGATCCTGCAGAACATGGCAGCCCATTTGGG
TCTTCCTGGAGACTCATGATGGACACCCACAGCTGACCAACCGCGAGTGCTCTATGCAG
CCACCTTTCTTCTCTTCCCCCTCAATGTGCTGGTGGGTGCCATGGTGGCCACCTGGCGAG
TGCTCCTCTCTGCCCTCTACAACGCCATCCACCTTGGCCAGATGGACCTCAGCCTGCTGC
CACCGAGAGCCGCCACTCTCGACCCCGGCTACTACACGTACCGAAACTTCTTGAAGATTG
AAGTCAGCCAGTCGCATCCAGCCATGACAGCCTTCTGCTCCCTGCTCCTGCAAGCGCAGA
GCCTCCTACCCAGGACCATGGCAGCCCCCAGGACAGCCTCAGACCAGGGGAGGAAGACG
AAGGGATGCAGCTGTACAGACAAAGGACTCCATGGCCAAGGGAGCTAGGCCCGGGGCCA
GCCGCGGCAGGGCTCGCTGGGGTCTGGCCTACAGCTGCTGCACAACCAACCTGCAGG
TCTTCGCAAGACGGCCCTGTGGGTGCCAATGGTGCCAGCCCT**GAGGGCAGGGAAGGT**
CAACCCACCTGCCATCTGTGCTGAGGCATGTTCTGCCTACCATCCTCCTCCCTCCCCG
GCTCTCTCCAGCATCACACAGCCATGCAGCCAGCAGGTCTCCGGATCACTGTGGTT
GGGTGGAGGTCTGTCTGCACTGGGAGCCTCAGGAGGGCTCTGCTCCACCCACTTGGCTAT
GGGAGAGCCAGCAGGGTTCTGGAGAAAAAACTGGTGGGTTAGGGCCTTGGTCCAGGA
GCCAGTTGAGCCAGGGCAGCCACATCCAGGCGTCTCCCTACCCTGGCTCTGCCATCAGCC
TTGAAGGGCCTCGATGAAGCCTTCTTGGAAACCACTCCAGCCAGCTCCACCTCAGCCTT
GGCCTTCAGCTGTGGAAGCAGCCAAGGCACTTCTCACCCCTCAGCGCCACGGACCTC
TCTGGGGAGTGGCCGGAAGCTCCCGGGCTCTGGCCTGCAGGGCAGCCCAAGTCATGAC

TCAGACCAGGTCCCACACTGAGCTGCCACACTCGAGAGCCAGATATTTTGTAGTTTT ATGCCTTTGGCTATTATGAAAGAGGTTAGTGTGTTCCTG
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The NOV8c protein encoded by SEQ ID NO:31 has 667 amino acid residues, and is presented using the one-letter code in Table 8F (SEQ ID NO:32). The SignalP, Psort and Hydropathy profile for the Retinoic Acid-Responsive Protein-like protein predict that this sequence has a signal peptide and is likely to be localized at the plasma membrane with a certainty of 0.6000. NOV8b is also likely localized to the Golgi body (certainty = 0.4000); endoplasmic reticulum (membrane) (certainty = 0.3000); and microbody (peroxisome) (certainty = 0.3000). The first 8 amino acids are more likely to be cleaved as a signal peptide based on the SignalP result (*i.e.*, between the slash in the sequence AGN-QT).

Table 8F. Encoded NOV8c protein sequence (SEQ ID NO:30).

MSSQPAGNQTSFGATEDYSYGSWYIDEPQGGEEELQPEGEVPSCHTSIPPGLYHACLASLS ILVLLLLLAMLVRRRLWPDVCVRGRLPSPVDFLAGDRPRAVPAAVFMILLSSLCLLLPD EDALPFLTASAPSQDGKTEAPRGAWKILGLFYAAALYPLAACATAGHTAAHLLGSTLS WAHLGVQVWQRAECPQVPKIYKYSSLASLPLLLGLGFLSLWYPVQLVRSFSRRTGAGSK GLQSSYSEYLRNLLCRKKLGSSYHTSKHGFLSWARVCLRHCIYTPQPGFHLPLKLVLSA TLTGTAIYQVALLLVGVVPTIQKVRAGVTTDVSYLLAGFGIVLSEDKQEVVELVKHHLW ALEVCYISALVLSCLLTFLVLMRSLVTHRTNLRALHRGAALDLSPLHRSPHPSRQAIFCW MSFSAYQTAFICLGLLVQQIIFFLGTTALAFLVLMPLVHGRNLLLFRSLESSWPFWLTLA LAVILQNMAAHWVFLETHDGHQPQLTNRRLVYAATFLLFPLNVLVGAMVATWRVLLSALYN AIHLGQMDLSLLPPRAATLDPGYTYRNFLEKIEVSQSHPAMTAFCSLLLQAQSLLPRTMA APQDSLRLPGEDEGMQLLQTKDSMAKGARPGASRGRRARWGLAYTLLHNPTLQVERKTALL GANGAQP
--

The disclosed NOV8b disclosed in this invention is expressed in at least the following tissues: Heart, Thyroid, Lymphoid tissue, Lymph node, Brain, Pituitary Gland, Temporal Lobe, Cervix, Ovary. Expression information was derived from the tissue sources of the sequences that were included in the derivation of the sequence of NOV8c (CuraGen Acc. No. CG52276-04).

NOV8c maps to chromosome 15.

As used herein, any reference to NOV8 encompasses NOV8a, NOV8b, and NOV8c. A comparison of the NOV8 nucleic acid sequences is given in Table 8G. A comparison of the NOV8 amino acid sequences is given in Table 8H.

Table 8G. Comparison of NOV8 Nucleic Acid Sequences

	10	20	30	40	50	60
NOV8a
NOV8b	-----	-----	-----	-----	-----	-----
NOV8c	-----	-----	-----	-----	-----	-----
	70	80	90	100	110	120
NOV8a
NOV8b
NOV8c
	130	140	150	160	170	180
NOV8a
NOV8b
NOV8c
	190	200	210	220	230	240
NOV8a
NOV8b
NOV8c
	C A					
	250	260	270	280	290	300
NOV8a
NOV8b
NOV8c
	310	320	330	340	350	360
NOV8a
NOV8b
NOV8c
	A					
	370	380	390	400	410	420
NOV8a
NOV8b
NOV8c
	430	440	450	460	470	480
NOV8a
NOV8b	-----	-----	-----	-----	-----	-----
NOV8c	-----	-----	-----	-----	-----	-----
	490	500	510	520	530	540
NOV8a
NOV8b
NOV8c
	550	560	570	580	590	600
NOV8a
NOV8b
NOV8c
	610	620	630	640	650	660
NOV8a
NOV8b
NOV8c
	670	680	690	700	710	720
NOV8a
NOV8b

NOV8c						
	730	740	750	760	770	780

NOV8a						
NOV8b						
NOV8c		A				
	790	800	810	820	830	840

NOV8a						
NOV8b						
NOV8c			---			
	850	860	870	880	890	900

NOV8a						
NOV8b						
NOV8c						
	910	920	930	940	950	960

NOV8a						
NOV8b						
NOV8c					G	
	970	980	990	1000	1010	1020

NOV8a						
NOV8b						
NOV8c						
	1030	1040	1050	1060	1070	1080

NOV8a						
NOV8b						
NOV8c						
	1090	1100	1110	1120	1130	1140

NOV8a						
NOV8b						
NOV8c						
	1150	1160	1170	1180	1190	1200

NOV8a						
NOV8b						
NOV8c						
	1210	1220	1230	1240	1250	1260

NOV8a						
NOV8b						
NOV8c						
	1270	1280	1290	1300	1310	1320

NOV8a						
NOV8b						
NOV8c						
	1330	1340	1350	1360	1370	1380

NOV8a						
NOV8b						
NOV8c		G				
	1390	1400	1410	1420	1430	1440

NOV8a						
NOV8b						
NOV8c						

	1450	1460	1470	1480	1490	1500
NOV8a					
NOV8b	---	-----				
NOV8c	G	TCT	GACTTTGGCCCTGGC			
	1510	1520	1530	1540	1550	1560
NOV8a					
NOV8b						
NOV8c						
	1570	1580	1590	1600	1610	1620
NOV8a					
NOV8b						
NOV8c						
	1630	1640	1650	1660	1670	1680
NOV8a					
NOV8b						
NOV8c						
	1690	1700	1710	1720	1730	1740
NOV8a					
NOV8b						
NOV8c			C			
	1750	1760	1770	1780	1790	1800
NOV8a					
NOV8b						
NOV8c						
	1810	1820	1830	1840	1850	1860
NOV8a					
NOV8b						
NOV8c						
	1870	1880	1890	1900	1910	1920
NOV8a					
NOV8b						
NOV8c		G				
	1930	1940	1950	1960	1970	1980
NOV8a					
NOV8b						
NOV8c						
	1990	2000	2010	2020	2030	2040
NOV8a					
NOV8b					-----	
NOV8c					GGGCAGGGAA	
	2050	2060	2070	2080	2090	2100
NOV8a					
NOV8b	-----					
NOV8c	GGTCAACCCACCTGCCCATCTGTGCTGAGGCATGTTCTCTGCCTACCATCCTCCTCCCTCC					
	2110	2120	2130	2140	2150	2160
NOV8a					
NOV8b	-----					
NOV8c	CCGGCTCTCCTCCCAGCATCACACCAGCCATGCAGCCAGCAGGTCTCCGGATCACTGTG					

[illegible]

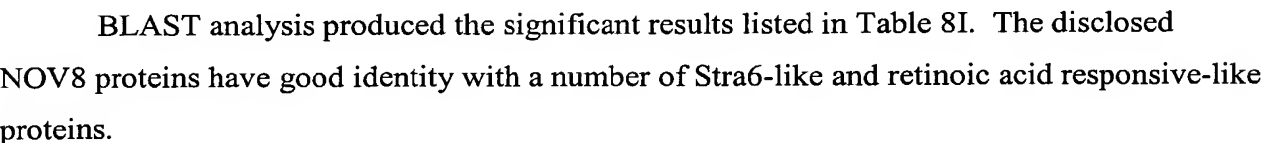


Table 8I. BLAST results for NOV8					
Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
gi 13560966 gb AAK30289.1 AF352728.1 (AF352728)	STRA6 isoform 1 (<i>Homo sapiens</i>)	667	535/668 (80%)	536/668 (80%) Gaps = 16/668 (2%)	0.0

gi 13560968 gb AAK30290.1 AF352729_1 (AF352729)	STRA6 isoform 2 (<i>Homo sapiens</i>)	658	522/668 (78%)	527/668 (78%) Gaps = 25/668 (3%)	0.0
gi 11641295 ref NP_071764.1 ; gi 10434086 dbj BAB14122.1 (AK022603)	hypothetical protein FLJ12541 similar to Stra6; unnamed protein product (<i>Homo sapiens</i>)	560	462/561 (82%)	463/561 (82%) Gaps = 16/561 (2%)	0.0
gi 6678171 ref NP_033317.1 ; gi 3126975 gb AAC16016.1 (AF062476)	stimulated by retinoic acid gene 6; retinoic acid- responsive protein; STRA6 (<i>Mus musculus</i>)	670	396/672 (58%)	447/672 (65%) Gaps = 21/672 (3%)	0.0
gi 13651719 ref XP_016576.1	hypothetical protein FLJ12541 similar to Stra6 (<i>Homo sapiens</i>)	188	174/180	174/180 (96%) Gaps = 6/180 (3%)	4e-86

This information is presented graphically in the multiple sequence alignment given in Table 8J (with NOV8a being shown on line 1, NOV8b being shown on line 2, and NOV8c being shown on line 3) as a ClustalW analysis comparing NOV8 with related protein sequences.

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Table 8J. Information for the ClustalW proteins:

- 1) NOV8a (SEQ ID NO:28)
- 2) NOV8b (SEQ ID NO:30)
- 3) NOV8c (SEQ ID NO:32)
- 4) gi|13560966| (SEQ ID NO:67)
- 5) gi|13560968| (SEQ ID NO:68)
- 6) gi|11641295| (SEQ ID NO:69)
- 7) gi|6678171| (SEQ ID NO:70)
- 8) gi|13651719| (SEQ ID NO:71)

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		10	20	30	40	50	60
						
NOV8a		MSSQPAGNOTSPGATEDYSYGSWYIDEPOGGEELOPEGEVPSCHTSTPPGLYHACLASL					
NOV8b		MSSQPAGNOTSPGATEDYSYGSWYIDEPOGGEELOPEGEVPSCHTSTPPGLYHACITPL					
NOV8c		MSSQPAGNOTSPGATEDYSYGSWYIDEPOGGEELOPEGEVPSCHTSTPPGLYHACLASL					
gi 13560966		MSSQPAGNOTSPGATEDYSYGSWYIDEPOGGEELOPEGEVPSCHTSTPPGLYHACLASL					
gi 13560968		MSSQPAGNOTSPGATEDYSYGSWYIDEPOGGEELOPEGEVPSCHTSTPPGLYHACLASL					
gi 11641295		-----					
gi 6678171		YENGASENGSQTSSGVTDDYSWYIEEHLAEFYDPEGVITLLQLTAPFAILLACLASL					
gi 13651719		-----					
		70	80	90	100	110	120
						
NOV8a		ILVLIILIAMLVRRROLWPDCVRGRPGILPSPVDFLAGIRPRAPVAAPVFMVLLSSLCLLLPI					

NOV8b	ILVILLIAMLVRRRLWPDVGRGRGPLSPVDFLAGIRPRAVPAAVFMVLLSSICLLLP
NOV8c	ILVILLIAMLVRRRLWPDVGRGRGPLSPVDFLAGIRPRAVPAAVFMVLLSSICLLLP
gi 13560966	ILVILLIAMLVRRRLWPDVGRGRGPLSPVDFLAGIRPRAVPAAVFMVLLSSICLLLP
gi 13560968	ILVILLIAMLVRRRLWPDVGRGRGPLSPVDFLAGIRPRAVPAAVFMVLLSSICLLLP
gi 11641295	ILVILLIAMLVRRRLWPDVGRGRGPLSPVDFLAGIRPRAVPAAVFMVLLSSICLLLP
gi 6678171	ILVILLIAMLVRRRLWPDVGRGRGPLSPVDFLAGIRPRAVPAAVFMVLLSSICLLLP
gi 13651719	ILVILLIAMLVRRRLWPDVGRGRGPLSPVDFLAGIRPRAVPAAVFMVLLSSICLLLP
	130 140 150 160 170 180
NOV8a	EDALPFLTLASAPSDGKTEAPRGAWKILGLFYAALYYPIAACATAGHTAAHLLGSTL
NOV8b	EDALPFLTLASAPSDGKTEAPRGAWKILGLFYAALYYPIAACATAGHTAAHLLGSTL
NOV8c	EDALPFLTLASAPSDGKTEAPRGAWKILGLFYAALYYPIAACATAGHTAAHLLGSTL
gi 13560966	EDALPFLTLASAPSDGKTEAPRGAWKILGLFYAALYYPIAACATAGHTAAHLLGSTL
gi 13560968	EDALPFLTLASAPSDGKTEAPRGAWKILGLFYAALYYPIAACATAGHTAAHLLGSTL
gi 11641295	EDALPFLTLASAPSDGKTEAPRGAWKILGLFYAALYYPIAACATAGHTAAHLLGSTL
gi 6678171	EDALPFLTLASAPSDGKTEAPRGAWKILGLFYAALYYPIAACATAGHTAAHLLGSTL
gi 13651719	EDALPFLTLASAPSDGKTEAPRGAWKILGLFYAALYYPIAACATAGHTAAHLLGSTL
	190 200 210 220 230 240
NOV8a	WAHLGVQVWQRAECPOVPKIYKYYSLLASLPLLLGLGFLSLWYPVQLVRSFSRRTGAG
NOV8b	WAHLGVQVWQRAECPOVPKIYKYYSLLASLPLLLGLGFLSLWYPVQLVRSFSRRTGAG
NOV8c	WAHLGVQVWQRAECPOVPKIYKYYSLLASLPLLLGLGFLSLWYPVQLVRSFSRRTGAG
gi 13560966	WAHLGVQVWQRAECPOVPKIYKYYSLLASLPLLLGLGFLSLWYPVQLVRSFSRRTGAG
gi 13560968	WAHLGVQVWQRAECPOVPKIYKYYSLLASLPLLLGLGFLSLWYPVQLVRSFSRRTGAG
gi 11641295	WAHLGVQVWQRAECPOVPKIYKYYSLLASLPLLLGLGFLSLWYPVQLVRSFSRRTGAG
gi 6678171	WAHLGVQVWQRAECPOVPKIYKYYSLLASLPLLLGLGFLSLWYPVQLVRSFSRRTGAG
gi 13651719	WAHLGVQVWQRAECPOVPKIYKYYSLLASLPLLLGLGFLSLWYPVQLVRSFSRRTGAG
	250 260 270 280 290 300
NOV8a	GLOSSYSEFYLRNLLCRKKILSCSYHTSKHGFLSWARVCLRHCIYTPQPGFHLPLKVL
NOV8b	GLOSSYSEFYLRNLLCRKKILSCSYHTSKHGFLSWARVCLRHCIYTPQPGFHLPLKVL
NOV8c	GLOSSYSEFYLRNLLCRKKILSCSYHTSKHGFLSWARVCLRHCIYTPQPGFHLPLKVL
gi 13560966	GLOSSYSEFYLRNLLCRKKILSCSYHTSKHGFLSWARVCLRHCIYTPQPGFHLPLKVL
gi 13560968	GLOSSYSEFYLRNLLCRKKILSCSYHTSKHGFLSWARVCLRHCIYTPQPGFHLPLKVL
gi 11641295	GLOSSYSEFYLRNLLCRKKILSCSYHTSKHGFLSWARVCLRHCIYTPQPGFHLPLKVL
gi 6678171	GLOSSYSEFYLRNLLCRKKILSCSYHTSKHGFLSWARVCLRHCIYTPQPGFHLPLKVL
gi 13651719	GLOSSYSEFYLRNLLCRKKILSCSYHTSKHGFLSWARVCLRHCIYTPQPGFHLPLKVL
	310 320 330 340 350 360
NOV8a	ATLTGTAIYQVALLLVGVVPTIQKVRAGVTTDVSYLLAGFGIVLSEDKQEVVVLVKHHI
NOV8b	ATLTGTAIYQVALLLVGVVPTIQKVRAGVTTDVSYLLAGFGIVLSEDKQEVVVLVKHHI
NOV8c	ATLTGTAIYQVALLLVGVVPTIQKVRAGVTTDVSYLLAGFGIVLSEDKQEVVVLVKHHI
gi 13560966	ATLTGTAIYQVALLLVGVVPTIQKVRAGVTTDVSYLLAGFGIVLSEDKQEVVVLVKHHI
gi 13560968	ATLTGTAIYQVALLLVGVVPTIQKVRAGVTTDVSYLLAGFGIVLSEDKQEVVVLVKHHI
gi 11641295	ATLTGTAIYQVALLLVGVVPTIQKVRAGVTTDVSYLLAGFGIVLSEDKQEVVVLVKHHI
gi 6678171	ATLTGTAIYQVALLLVGVVPTIQKVRAGVTTDVSYLLAGFGIVLSEDKQEVVVLVKHHI
gi 13651719	ATLTGTAIYQVALLLVGVVPTIQKVRAGVTTDVSYLLAGFGIVLSEDKQEVVVLVKHHI
	370 380 390 400 410 420
NOV8a	HALEVCIYSAIVLSCLLTFVLVLRSLVTHRTNLRALIRGAALDLSPLHRSRPHSRQATFC
NOV8b	HALEVCIYSAIVLSCLLTFVLVLRSLVTHRTNLRALIRGAALDLSPLHRSRPHSRQATFC

NOV8c	VALEVCYISALVLSCLLTFLVIMRSLVTHRTNLRALHGAALDLSPLHRSHPSPSQATFC
gi 13560966	VALEVCYISALVLSCLLTFLVIMRSLVTHRTNLRALHGAALDLSPLHRSHPSPSQATFC
gi 13560968	VALEVCYISALVLSCLLTFLVIMRSLVTHRTNLRALHGAALDLSPLHRSHPSPSQATFC
gi 11641295	VALEVCYISALVLSCLLTFLVIMRSLVTHRTNLRALHGAALDLSPLHRSHPSPSQATFC
gi 6678171	TVFACTYSALVLSCLLTFLVIMRSLVTHRTNLRALHGAALDLSPLHRSHPSPSQATFC
gi 13651719	-----MRSLVTHRTNLRALHGAALDLSPLHRSHPSPSQATFC
	430 440 450 460 470 480
NOV8a	MSFSAYQTAFICLGLLVQOIIFELGTTALAFVLMFVHGRNLLFRSLESSW----
NOV8b	MSFSAYQTAFICLGLLVQOIIFELGTTALAFVLMFVHGRNLLFRSLESSW----
NOV8c	MSFSAYQTAFICLGLLVQOIIFELGTTALAFVLMFVHGRNLLFRSLESSWPFWLT
gi 13560966	MSFSAYQTAFICLGLLVQOIIFELGTTALAFVLMFVHGRNLLFRSLESSWPFWLT
gi 13560968	MSFSAYQTAFICLGLLVQOIIFELGTTALAFVLMFVHGRNLLFRSLESSWPFWLT
gi 11641295	MSFSAYQTAFICLGLLVQOIIFELGTTALAFVLMFVHGRNLLFRSLESSWPFWLT
gi 6678171	MSFSAYQTAFICLGLLVQOIIFELGTTALAFVLMFVHGRNLLFRSLESSWPFWLT
gi 13651719	MSFSAYQTAFICLGLLVQOIIFELGTTALAFVLMFVHGRNLLFRSLESSWPFWLT
	490 500 510 520 530 540
NOV8a	-WLITLONMAAHWVFLETHDGHPOLTNRRVLYAATFLLFPLNVLVGAMVATWRVLLSAL
NOV8b	-WLITLONMAAHWVFLETHDGHPOLTNRRVLYAATFLLFPLNVLVGAMVATWRVLLSAL
NOV8c	ALAVILONMAAHWVFLETHDGHPOLTNRRVLYAATFLLFPLNVLVGAMVATWRVLLSAL
gi 13560966	ALAVILONMAAHWVFLETHDGHPOLTNRRVLYAATFLLFPLNVLVGAMVATWRVLLSAL
gi 13560968	ALAVILONMAAHWVFLETHDGHPOLTNRRVLYAATFLLFPLNVLVGAMVATWRVLLSAL
gi 11641295	ALAVILONMAAHWVFLETHDGHPOLTNRRVLYAATFLLFPLNVLVGAMVATWRVLLSAL
gi 6678171	ALAVILONMAAHWVFLETHDGHPOLTNRRVLYAATFLLFPLNVLVGAMVATWRVLLSAL
gi 13651719	ALAVILONMAAHWVFLETHDGHPOLTNRRVLYAATFLLFPLNVLVGAMVATWRVLLSAL
	550 560 570 580 590 600
NOV8a	NATHLGQMDLSLLPPRAATLDPGYYTYRNFLEKIEVSQSHPAMTAFCSLLLOAQSLLPRTH
NOV8b	NATHLGQMDLSLLPPRAATLDPGYYTYRNFLEKIEVSQSHPAMTAFCSLLLOAQSLLPRTH
NOV8c	NATHLGQMDLSLLPPRAATLDPGYYTYRNFLEKIEVSQSHPAMTAFCSLLLOAQSLLPRTH
gi 13560966	NATHLGQMDLSLLPPRAATLDPGYYTYRNFLEKIEVSQSHPAMTAFCSLLLOAQSLLPRTH
gi 13560968	NATHLGQMDLSLLPPRAATLDPGYYTYRNFLEKIEVSQSHPAMTAFCSLLLOAQSLLPRTH
gi 11641295	NATHLGQMDLSLLPPRAATLDPGYYTYRNFLEKIEVSQSHPAMTAFCSLLLOAQSLLPRTH
gi 6678171	NATHLGQMDLSLLPPRAATLDPGYYTYRNFLEKIEVSQSHPAMTAFCSLLLOAQSLLPRTH
gi 13651719	NATHLGQMDLSLLPPRAATLDPGYYTYRNFLEKIEVSQSHPAMTAFCSLLLOAQSLLPRTH
	610 620 630 640 650 660
NOV8a	AAPQDSLPGEEDEGMQLLOTKDSMAKGARPGASRGARWGLAYTLHNPTLOVFRKTAI
NOV8b	AAPQDSLPGEEDEGMQLLOTKDSMAKGARPGASRGARWGLAYTLHNPTLOVFRKTAI
NOV8c	AAPQDSLPGEEDEGMQLLOTKDSMAKGARPGASRGARWGLAYTLHNPTLOVFRKTAI
gi 13560966	AAPQDSLPGEEDEGMQLLOTKDSMAKGARPGASRGARWGLAYTLHNPTLOVFRKTAI
gi 13560968	AAPQDSLPGEEDEGMQLLOTKDSMAKGARPGASRGARWGLAYTLHNPTLOVFRKTAI
gi 11641295	AAPQDSLPGEEDEGMQLLOTKDSMAKGARPGASRGARWGLAYTLHNPTLOVFRKTAI
gi 6678171	AAPQDSLPGEEDEGMQLLOTKDSMAKGARPGASRGARWGLAYTLHNPTLOVFRKTAI
gi 13651719	AAPQDSLPGEEDEGMQLLOTKDSMAKGARPGASRGARWGLAYTLHNPTLOVFRKTAI
	670
NOV8a	LGANGAQL--
NOV8b	LGANGAQL--
NOV8c	LGANGAQL--

gi 13560966	LGANGAOF--
gi 13560968	LGANGAOF--
gi 11641295	LGANGAOF--
gi 6678171	TSKANGTQP
gi 13651719	-----

Other BLAST results include sequences from the Patp database, which is a proprietary database that contains sequences published in patents and patent publications. Patp results include those listed in Table 8K.

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Table 8K. Patp alignments of NOV8					
Sequences producing High-scoring Segment Pairs:				Smallest Sum	
		Reading Frame	High Score	Prob. P (N)	
Patp:AAB53256	Human colon cancer antigen protein, 178 aa	+1	807	6.1e-83	
Patp:AAW88559	Secreted protein encoded by gene 26, 88 aa	+1	441	1.5e-40	

For example, a BLAST against patp:AAB53256, a 178 amino acid Human colon cancer antigen protein (WO/55351), produced good identity, $E = 6.1e-83$. Moreover, a BLAST against patp:AAW88559, a 88 amino acid secreted protein encoded by gene 26 clone HTDAF28 (WO98/54963) from *Homo sapiens*, also produced good identity, $E=1.5e-40$.

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Retinoic acid plays important roles in development, growth and differentiation by regulating the expression of target genes. A new retinoic acid-inducible gene, Stra6, has been identified in P19 embryonal carcinoma cells using a subtractive hybridization cDNA cloning technique. Stra6 codes for a very hydrophobic membrane protein of a new type, which does not display similarities with previously characterized integral membrane proteins. Stra6, which exhibits a specific pattern of expression during development and in the adult, is strongly expressed at the level of blood-organ barriers. Interestingly, in testis Sertoli cells, Stra6 has a spermatogenic cycle-dependent expression, which is lost in testes of RAR alpha null mutants where Stra6 is expressed in all tubules. The Stra6 protein may be a component of an as yet unidentified transport machinery. See generally *Mech Dev* 63(2):173-86 (1997); PMID: 9203140, UI: 97346723.

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Using a differential subtractive hybridization cloning procedure Stra6 has recently been identified as a novel retinoic acid-induced gene in murine P19 embryonal carcinoma cells. The

putative amino acid sequence of Stra6 shows no similarity with previously characterised proteins. The pattern of expression of Stra6 transcripts during mouse limb development as revealed by *in situ* hybridization has been reported. In 8.5-9.0 days post-coitum (dpc) embryos, Stra6 was expressed in the lateral plate mesenchyme prior to limb bud outgrowth. By 9.5 dpc, expression was restricted to the proximal and dorsal forelimb bud mesoderm. Over the next 2 gestational days, Stra6 expression was specific of the dorsal mesoderm of the undifferentiated forelimb and hindlimb buds with the exception of their distal-most region or progress zone. A novel proximal-ventral expression domain appeared, however, by 11.0-11.5 dpc. Stra6 also remained expressed in the flank mesoderm. From 11.5-13.5 dpc, Stra6 expression was restricted to the superficial mesenchyme surrounding the chondrogenic blastemas, and progressively extended until the distal extremities of the limbs upon disappearance of the progress zone. Progressive restriction of Stra6 expression to perichondrium and developing muscles was seen at 13.5-14.5 dpc. Upon the initiation of endochondral ossification (15.5-16.5 dpc), Stra6 expression was limited to the area of perichondrium opposing cells of high metabolic and proliferative activity (the elongation zone). This suggests that Stra6 may play a role in early dorsoventral limb patterning and later in the control of endochondral ossification. *See generally Dev Genet* 19(1):66-73 (1996); PMID: 8792610, UI: 96384726.

Disruption of retinoic acid receptor (RAR) gamma in F9 embryonal carcinoma cells leads to aberrant differentiation and reduced activation of expression of several all-trans-retinoic acid (RA)-induced genes. The expression of several additional RA-responsive genes in RAR alpha- and RAR gamma-null F9 cells was analyzed. The RA-induced activation of Cdx1, Gap43, Stra4, and Stra6 was specifically impaired in RAR gamma-null cells, supporting the idea that each RAR may regulate distinct subsets of target genes. To further investigate the role of RAR gamma in F9 cell differentiation, "rescue" cell lines reexpressing RAR gamma 2 or overexpressing either RAR alpha 1 or RAR beta 2 were established in RAR gamma-null cells. Reexpression of RAR gamma or overexpression of RAR alpha restored both target-gene activation and the differentiation potential. In contrast, over-expression of RAR beta only poorly restored differentiation, although it could replace RAR gamma for the activation of target genes. *See generally, Proc Natl Acad Sci U S A* 92(17):7854-58 (1995); PMID: 7644503, UI: 95372377.

Carcinogenesis involves inactivation or subversion of the normal controls of proliferation, differentiation, and apoptosis (Hurst et.al. *Adv Exp Med Biol* 462:449-67 (1999)).

However, these controls are robust, redundant, and interlinked at the gene expression levels, regulation of mRNA lifetimes, transcription, and recycling of proteins. One of the central systems of control of proliferation, differentiation and apoptosis is retinoid signaling. The hRAR alpha nuclear receptor occupies a central position with respect to induction of gene transcription in that when bound to appropriate retinoid ligands, its homodimers and heterodimers with hRXR alpha regulate the transcription of a number of retinoid-responsive genes. These include genes in other signaling pathways, so that the whole forms a complex network. It has been shown that simple, cause-effect interpretations in terms of hRAR alpha gene transcription being the central regulatory event would not describe the retinoid-responsive gene network.

A set of cultured bladder-derived cells representing different stages of bladder tumorigenesis formed a model system. It consisted of two immortalized bladder cell lines (HUC-BC and HUC-PC), one squamous cell carcinoma cell line (SCaBER), one papilloma line (RT4), and 4 transitional cell carcinomas (TCC-Sup, 5637, T24, J82) of varying stages and grades. This set of cells was used to model the range of behaviors of bladder cancers. Relative gene expression before (constitutive) and after treatment with 10 microM all-trans-retinoic acid (aTRA) was measured for androgen and estrogen receptor; a set of genes involved with retinoid metabolism and action, hRAR alpha and beta, hRXR alpha and beta CRBP, CRABP I and II; and for signaling genes that are known to be sensitive to retinoic acid, EGFR, cytokine MK, ICAM I and transglutaminase. The phenotype for inhibition of proliferation and for apoptotic response to both aTRA and the synthetic retinoid 4-HPR was determined. Transfection with a CAT-containing plasmid containing an aTRA-sensitive promoter was used to determine if the common retinoic acid responsive element (RARE)-dependent pathway for retinoid regulation of gene expression was active. Each of the genes selected is known from previous studies to react to aTRA in a certain way, either by up- or down-regulation of the message and protein. A complex data set not readily interpretable by simple cause and effect was observed.

While all cell lines expressed high levels of the mRNAs for hRXR alpha and beta that were not altered by treatment with exogenous aTRA, constitutive and stimulated responses of the other genes varied widely among the cell lines. For example, CRABP I was not expressed by J82, T24, 5637 and RT4, but was expressed at low levels that did not change in SCaBER and at moderate levels that decreased, increased, or decreased sharply in HUC-BC, TCC-Sup and HUC-PC, respectively. The expression of hRAR alpha, which governs the expression of

many retinoid-sensitive genes, was expressed at moderate to high levels in all cell lines, but in some it was sharply upregulated (TCC-Sup, HUC-PC and J82), remained constant (5637 and HUC-BC), or was down-regulated (SCaBER, T24 and RT4). The phenotypes for inhibition of proliferation showed no obvious relationship to the expression of any single gene, but cell lines that were inhibited by a TRA (HUC-BC and TCC-Sup) were not sensitive to 4-HPR, and vice versa. One line (RT4) was insensitive to either retinoid. Transfection showed very little retinoid-stimulated transfection of the CAT reporter gene with RT4 or HUC-PC. About 2-fold enhancement transactivation was observed with SCaBER, HUC-BC, J82 and T24 cells and 3-8 fold with 5637, TCC-Sup cells. In HUC-BC, a G to T point mutation was found at position 606 of the hRAR alpha gene. This mutation would substitute tyrosine for asparagine in a highly conserved domain.

These data indicate that retinoid signaling is probably a frequent target of inactivation in bladder carcinogenesis. The presence and functionality of retinoid signaling pathways in human urinary bladder carcinoma and SV40-immortalized uroepithelial cell lines has been examined. (See Waliszewski, et.al.; Mol Cell Endocrinol 148(1-2):55-65 (1999)). Only two of eight cell lines were proliferation-inhibited by 10 microM of either all-trans or 13-cis-retinoic acid. Transactivation of the CAT gene under control of a retinoid-responsive element demonstrated functionality of the signaling pathway in both sensitive cell lines and four of six resistant cell lines. Relative RT-PCR analysis of a panel of retinoid-responsive and inducible genes demonstrated changes in expression levels of all the genes in response to-retinoic acid treatment together with numerous aberrations dysregulations.

Retinoid signaling may be a target for inactivation during tumorigenesis by uncoupling gene expression, proliferation and differentiation. Therefore retinoids are more likely to be effective for chemoprevention than for treatment of bladder carcinomas. The proliferative effects of retinoids were examined in the MC-26 and LoVo colon adenocarcinoma cell lines (See Stewart, et.al. Exp Cell Res 233(2):321-29 (1997)). The proliferation of the LoVo cell line was not altered in the presence of the retinoids all trans-retinoic acid (atRA) and 9-cis-retinoic acid (9-cis-RA). Both retinoids, however, stimulated the growth, as measured by cell proliferation, of MC-26 cells. atRA and 9-cis-RA were equipotent in increasing MC-26 cell proliferation, suggesting that the growth stimulation is mediated by one or more retinoic acid receptors (RARs). To determine the RAR, which might be responsible for this growth stimulatory effect, the RAR subtypes which were present in both cell lines were characterized.

mRNA for the RAR alpha, RAR beta, and RAR gamma were detected in the MC-26 cell. Of the RARs present in MC-26 cells, the RAR alpha does not mediate the growth stimulatory effects of retinoids, for a selective RAR alpha antagonist was unable to prevent the retinoid-induced increase in MC-26 cell growth. RAR alpha, RAR beta, and RAR gamma mRNA are also expressed in the LoVo cell line; the lack of growth-stimulation by retinoids in LoVo cells, therefore, does not seem to be due to the absence of RARs.

The results obtained in these experiments demonstrate that the growth response elicited by retinoids can vary between colon cancer cells and that the differences in response may not be solely determined by the RAR subtypes which are expressed in a colon cancer cell line.

Retinoic acids (RAs), well characterized regulators of proliferation and differentiation, partly re-differentiate follicular thyroid carcinoma cell lines (FTC-133, FTC-238, and HTC-TSHr) as well as SV40-transfected immortalized thyroid cell lines (ori3 and 7751) (*See Schmutzler et.al Exp Clin Endocrinol Diabetes 104 Suppl 4:16-19 (1996)*). This is indicated by the stimulation of type I 5'-deiodinase and other differentiation markers. As demonstrated by RT-PCR, electrophoretic mobility shift, and [3H]-retinoic acid binding assays, thyroid carcinoma cell lines express RA receptor mRNAs and functional ligand- and DNA-binding receptor proteins able to mediate RA-dependent signal transduction. Together, these properties make these thyroid-derived cell lines useful *in vitro* models for studying the effects of an RA re-differentiation therapy of thyroid cancer.

The chemotherapeutic agent retinoic acid (RA) inhibits the proliferation and invasion of many tumor types (*See Vo et.al; Anticancer Res 18(1A):217-24 (1998)*). RA chemotherapy in head and neck squamous cell carcinoma (SCC) patients reduces recurrence and induces regression of premalignant lesions. The effects of RA are mediated by both cytoplasmic and nuclear proteins. In the nucleus, a family of ligand-dependent transcription factors, the retinoic acid receptors (RAR) and the retinoid X receptors (RXR), regulate target gene response to RA. In the cytoplasm, the cellular retinoic acid binding proteins I and II (CRABP) regulate intracellular RA concentration, transport, and metabolism. Alterations in CRABP expression have been shown to affect target gene response and the phenotype of cancer cells.

To elucidate the role of these proteins in mediating the RA response, target gene expression and malignant phenotype in SCC25 cells expressing an antisense CRABP II construct was examined. RA induced CRABP II mRNA levels 2 fold in SCC25 cells by transcriptional upregulation. Expression of the antisense construct reduced CRABP II

expression to undetectable levels. Inhibition of CRABP II expression resulted in significant downregulation of RA responsive genes. These reductions were the result of decreased transcription from RA responsive promoters. Surprisingly, clones expressing the antisense CRABP construct were less sensitive to RA mediated inhibition of proliferation. These clones
5 were also less invasive in an *in vitro* invasion assay, likely due to downregulation of matrix metalloproteinase activity.

CRABP II affects the transcription of RA responsive genes which regulate proliferation and invasion of head and neck SCCs. All-trans-retinoic acid (trans-RA) and other retinoids exert anticancer effects through two types of retinoid receptors, the RA receptors (RARs) and
10 retinoid X receptors (RXRs) (*See* Wu et.al.; Mol Cell Biol 17(11):6598-608 (1997)). Previous studies demonstrated that the growth-inhibitory effects of trans-RA and related retinoids are impaired in certain estrogen-independent breast cancer cell lines due to their lower levels of RAR alpha and RARbeta. In this study, we evaluated several synthetic retinoids for their ability to induce growth inhibition and apoptosis in both trans-RA-sensitive and trans-RA-resistant
15 breast cancer cell lines. RXR-selective retinoids, particularly in combination with RAR-selective retinoids, could significantly induce RARbeta and inhibit the growth and induce the apoptosis of trans-RA-resistant, RAR alpha-deficient MDA-MB-231 cells but had low activity against trans-RA-sensitive ZR-75-1 cells that express high levels of RAR alpha. Using gel retardation and transient transfection assays, the effects of RXR-selective retinoids on MDA-
20 MB-231 cells were most likely mediated by RXR-nur77 heterodimers that bound to the RA response element in the RARbeta promoter and activated the RARbeta promoter in response to RXR-selective retinoids. In contrast, growth inhibition by RAR-selective retinoids in trans-RA-sensitive, RAR alpha-expressing cells most probably occurred through RXR-RAR alpha heterodimers that also bound to and activated the RARbeta promoter. In MDA-MB-231 clones
25 stably expressing RAR alpha, both RARbeta induction and growth inhibition by RXR-selective retinoids were suppressed, while the effects of RAR-selective retinoids were enhanced. Together, the results demonstrate that activation of RXR can inhibit the growth of trans-RA-resistant MDA-MB-231 breast cancer cells and suggest that low cellular RAR alpha may regulate the signaling switch from RAR-mediated to RXR-mediated growth inhibition in breast
30 cancer cells.

The protein similarity information, expression pattern, and map location for the Retinoic Acid-Responsive Protein-like protein and nucleic acid disclosed herein suggest that this Retinoic

Acid-Responsive Protein may have important structural and/or physiological functions characteristic of the retinoic acid-responsive protein family. Therefore, the nucleic acids and proteins of the invention are useful in potential diagnostic and therapeutic applications and as a research tool. These include serving as a specific or selective nucleic acid or protein diagnostic and/or prognostic marker, wherein the presence or amount of the nucleic acid or the protein are to be assessed, as well as potential therapeutic applications such as the following: (i) a protein therapeutic, (ii) a small molecule drug target, (iii) an antibody target (therapeutic, diagnostic, drug targeting/cytotoxic antibody), (iv) a nucleic acid useful in gene therapy (gene delivery/gene ablation), and (v) a composition promoting tissue regeneration in vitro and in vivo (vi) biological defense weapon.

The nucleic acids and proteins of the invention are useful in potential diagnostic and therapeutic applications implicated in various diseases and disorders described below and/or other pathologies. For example, the compositions of the present invention will have efficacy for treatment of patients suffering from: Inflammation, Autoimmune disorders, Aging, cancer, Cardiomyopathy, Atherosclerosis, Hypertension, Congenital heart defects, Aortic stenosis, Atrial septal defect (ASD), Atrioventricular (A-V) canal defect, Ductus arteriosus, Pulmonary stenosis, Subaortic stenosis, Ventricular septal defect (VSD), valve diseases, Tuberosclerosis, Scleroderma, Obesity, Transplantation, Diabetes, Von Hippel-Lindau (VHL) syndrome, Pancreatitis, Endometriosis, Fertility, Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura, Immunodeficiencies, Graft versus host, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan as well as other diseases, disorders and conditions.

The novel nucleic acid encoding the NOV8 proteins, and the NOV8 proteins of the invention, or fragments thereof, may further be useful in diagnostic applications, wherein the presence or amount of the nucleic acid or the protein are to be assessed. These materials are further useful in the generation of antibodies that bind immunospecifically to the novel substances of the invention for use in therapeutic or diagnostic methods.

The novel nucleic acid encoding NOV8 proteins, and the NOV8 proteins of the invention, or fragments thereof, may further be useful in diagnostic applications, wherein the presence or amount of the nucleic acid or the protein are to be assessed. These materials are further useful in the generation of antibodies that bind immuno-specifically to the novel NOV8

substances for use in therapeutic or diagnostic methods. These antibodies may be generated according to methods known in the art, using prediction from hydrophobicity charts, as described in the "Anti-NOVX Antibodies" section below. For example the disclosed NOV8a and NOV8b proteins have multiple hydrophilic regions, each of which can be used as an immunogen. For example, hydrophilic regions are found from about amino acid 5 to about amino acid 50; from about amino acid 80 to about amino acid 100; from about amino acid 180 to about amino acid 190; from about amino acid 210 to about amino acid 280; from about amino acid 345 to about amino acid 350; from about amino acid 390 to about amino acid 410; from about amino acid 490 to about amino acid 500; from about amino acid 540 to about amino acid 560; and from about amino acid 595 to about amino acid 630. These novel proteins can also be used to develop assay system for functional analysis.

NOV9

NOV9 includes a novel protein encoded by a genomic DNA sequence and proteins similar to it, namely new proteins bearing sequence similarity to a protein encoded by thyroid regulated gene (TRG-like protein).

A novel nucleic acid was identified on chromosome 14 by TblastN using CuraGen Corporation's sequence file for TRG or homolog as run against the Genomic Daily Files made available by GenBank or from files downloaded from the individual sequencing centers. The nucleic acid sequence was predicted from the genomic file Genbank accession number: AL049870 by homology to a known TRG or homolog. Exons were predicted by homology and the intron/exon boundaries were determined using standard genetic rules. Exons were further selected and refined by means of similarity determination using multiple BLAST (for example, tBlastN, BlastX, and BlastN) searches, and, in some instances, GeneScan and Grail. Expressed sequences from both public and proprietary databases were also added when available to further define and complete the gene sequence. The DNA sequence was then manually corrected for apparent inconsistencies thereby obtaining the sequence designated SC108341967_A (NOV9) encoding the full-length protein.

In a search of CuraGen Corporation's proprietary human expressed sequence assembly database, assembly 108341967 (552 nucleotides) was identified as having >95% homology to this predicted gene sequence. SeqCalling is a differential expression and sequencing procedure that normalizes mRNA species in a sample, and is disclosed in U.S. Ser. No. 09/417,386, filed

Oct. 13, 1999, incorporated herein by reference in its entirety. This database is composed of the expressed sequences (as derived from isolated mRNA) from more than 96 different tissues. The mRNA is converted to cDNA and then sequenced. These expressed DNA sequences are then pooled in a database and those exhibiting a defined level of homology are combined into a single assembly with a common consensus sequence. The consensus sequence is representative of all member components. Since the disclosed NOV9 nucleic acid has >95% sequence identity with the CuraGen assembly, the nucleic acid of the invention represents an expressed gene sequence. This DNA assembly has 10 components.

A disclosed novel NOV9 nucleic acid is 1476 nucleotides long and is shown in Table 9A (SEQ ID NO:33). An ORF begins with an ATG initiation codon at nucleotides 1-3 and ends with a TAA codon at nucleotides 1474-1476. The start and stop codons are in bold letters in Table 9A.

Table 9A. NOV9 Nucleotide Sequence (SEQ ID NO:33)

ATGAAGGCAACTGCCTTTCCACAGAAGTCAAAGACTTGACCAAGAGAATCTGCACTGTTCTTATGGCCA
CTGCCCAAATGAAGGAGCATGAGAAAGACCCTGAAATGCTAACTGATCTCCAATGTAGCTTAGCCAAGTC
CTATGCAAGTATCCAGAGCTTAGGAAAACCTGGCTTGATAGCATGGCCAACATTCATGTAAAAATGGA
GATTTTTTCAGAGGCTGCAATGTGTATGTCCATGCAGCAGCTCTAGTTGCAGAGTTTCTTAAAAGTACCT
ACTGGAAAAGACCCAGAAGCTTCTTGGGACTTGTTTATACCATCCATGCAGCAGCTCTAGTTGCAGAGT
TTCTTCATTGAAAAAAAAATTTCTAATGGATGTTCAACCTTCAAGAAAATTACTCCCAATATAGTTGAA
GAAGGAGCAGTGAAAGAAGATGCTGGGATGATGGATGTCCATTATAGTGAAGAAGTTTTGCTGGAGTTGC
TAGAACAATGTGTGGATAGCTTATGGAAGGCAAACTTTATGAAATAATTTCTGAGATTTCCAAGTTGAT
CATTCCAATTTATGAGAAACATCCTGAGTTTGAGAACTTACTCAAGTTTATAGAACTCTTCAGGGAGCT
TACACAAAATTTCTGGAAAGTTATGCATACAAAAAAAAGAGAATTTTTTAGGCACTTTCTTCAGAGTT
GCCTTTATGGCCAGTCTTTTTTTGAAGAAGATGGAAGGAGTACATCTATAAAGAACCAAGCTCACTGG
CCTCTCAGAAATTTCCCTGAGACTTGTTAACTTTATGGTGAAAAATTTGGTATGGCGAATGTCAAAAA
ATTCAGGATACAGACGAGGTAAATACCAAAGAGTTTGATCCAAAATATGCTCATATACAAGTTACTTATG
TGAAGCCTTACTTTGATGACAAAGAACTCACAGAAAGAAAGACCGAGTTTGGAAGAAATCATAATATCAG
CAGATTTGTTTTGAGGCTCCTTACACTTTATCAGGCAAAAAGCAGGGTTGTACAGAAGAACAGTGCAAA
TGCCGTACAATCTTGACAACCTCAAAGTCATTTCCCTATGTGAAGAGGAGGATTCCTATTAAGTGTGAAC
AGCAGATTAATTTAAAACCAATGTATGTTGCCACTGATGAAATAAAAGATAAACTGCAGATCTGCAAAA
GCTTTGCTCCTCTGTTTATGTGGACATGATTCAACTCCAATTAAATTGCAGGGCTGTGTTTCCATGCAG
GTCAATGCTGGTCCATTAGCATATGCAGGGGCTTTCTTAAATGATAGCCAAGCTAGCAAGTATCCACCTA
GGAAAGTGAGTGAGTTGAAAGACATGTTTAGGAAATCCATACAAGCATGCAGCATTGCACTTGAACATAA
TGAGTGGCTAATTAAGAAGATCAAGTTGAGTACCATGAAGGGCTAAAGTCAAATTTAGAGACGTGGTA
AAATAA

A disclosed NOV9 protein encoded by SEQ ID NO:33 has 491 amino acid residues, and is presented using the one-letter code in Table 9B (SEQ ID NO:34). The SignalP, Psort and/or Hydropathy profile for NOV9 predict that NOV9 has a signal peptide and is likely to be localized in the mitochondrial matrix space with a certainty of 0.4555. Using SIGNALP analysis, it is predicted that the protein of the invention has a signal peptide with most likely cleavage site between residues 49 and 50 in the sequence CSLAKSYA-SI.

NOV9 was found to be expressed in at least the following tissues: testis, uterus, nervous system, lymphatic system, and muscle.

Table 9B. Encoded NOV9 protein sequence (SEQ ID NO:34).

MKATAFPTEVKDLTKRICTVLMATAQMKEHEKDPEMLTDLQCSLAKSYASIPELRKTWLDSEMAN
IHVKNMGDFSEAMCYVHAAALVAEFLKSTYWKKTQKLLGTCLYHPCSSSSSRVSSLKKKFPNGC
SPFKKITPNIVEEGAVKEDAGMMDVHYSEEVLLELLEQCVDLSWKAKLYEIISEISKLIPIYE
KHPEFEKLTQVYRTLQGAYTKILESAYKKKREFFRHFLQSCLYGQSFFEEEDGKEYIYKEPKLT
GLSEISLRVLKLYGEKFGMANVKKIQDTEVNTKEFDPKYAHIQVTYVKPYFDDKELTERKTEF
GRNHNISRFEAPYTLGSKKQGCTEEQCKCRTILTTSKSFYVKKRIPINCEQQINLKPIDVA
TDEIKDKTADLQKLCSSVYVDMIQQLKLQGCVMQVNAGPLAYAGAFNLDSQASKYPFRKVSE
LKDMFRKSIQACSI ALELNEWLIKEDQVEYHEGLKSNFRDVVK

The disclosed NOV9 protein (SEQ ID NO:34) has good identity with members of the TRG family. The identity information used for ClustalW analysis is presented in Table 9C.

Table 9C. BLAST results for NOV9

Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect	Gaps
gi 12657106 emb CAC27814.1 (AL161420)	bA155N3.2.1 (KIAA1058) (<i>Homo sapiens</i>)	1539	278/510 (54%)	343/510 (66%)	e-140	30/ 510 (5%)
gi 5689453 d bjl BAA83010.1 (AB028981)	KIAA1058 protein (<i>Homo sapiens</i>)	1534	278/510 (54%)	343/510 (66%)	e-140	30/ 510 (5%)
gi 7513980 p ir I60486; gi 550420 emb CAA48220.1 (X68101)	gene trg protein - rat (fragment); trg (<i>Rattus norvegicus</i>)	738	274/497 (55%)	333/497 (66%)	e-137	16/ 497 (3%)

gi 8923210 ref NP_060188.1 ; gi 7020173 dbj BAA91022.1 (AK000227)	hypothetical protein FLJ20220; unnamed protein product (<i>Homo sapiens</i>)	500	266/493 (53%)	334/493 (66%)	e-131	8/493 (1%)
gi 7022394 dbj BAA91583.1 (AK001253)	unnamed protein product (<i>Homo sapiens</i>)	415	191/368 (51%)	253/368 (67%)	7e-93	3/368 (0%)

This information is presented graphically in the multiple sequence alignment given in Table 9D (with NOV9 being shown on line 1) as a ClustalW analysis comparing NOV9 with related protein sequences.

5

Table 9D. Information for the ClustalW proteins:

- 1) NOV9 (SEQ ID NO:34)
- 2) gi|12657106| (SEQ ID NO:72)
- 3) gi|5689453| (SEQ ID NO:73)
- 4) gi|7513980| (SEQ ID NO:74)
- 5) gi|8923210| (SEQ ID NO:75)

10

	10	20	30	40	50	60
					
NOV9	-----					
gi 12657106	TLFKDASGNLDKNARFSAIYRQDSNKLSDMLKLLADFRKPEKMAKLPVILGNLDTITD					
gi 5689453	-----ASGNLDKNARFSAIYRQDSNKLSDMLKLLADFRKPEKMAKLPVILGNLDTITD					
gi 7513980	-----					
gi 8923210	-----					
	70	80	90	100	110	120
					
NOV9	-----					
gi 12657106	NVSSDFPNYVNSSYIPTKQFETCSKTPITFEVEEFVPCIPKHTQPYTIYTNHLYVYPKYL					
gi 5689453	NVSSDFPNYVNSSYIPTKQFETCSKTPITFEVEEFVPCIPKHTQPYTIYTNHLYVYPKYL					
gi 7513980	-----					
gi 8923210	-----					
	130	140	150	160	170	180
					
NOV9	-----					
gi 12657106	KYDSQKSFAKARNIAICIEFKDSDEEDSQPLKCIYGRPGGPVETRSAFAAVLHHHQNPEF					
gi 5689453	KYDSQKSFAKARNIAICIEFKDSDEEDSQPLKCIYGRPGGPVETRSAFAAVLHHHQNPEF					
gi 7513980	-----					
gi 8923210	-----					
	190	200	210	220	230	240
					
NOV9	-----					

gi 12657106	YDEIKIELPTQLHEKHHLLLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVT
gi 5689453	YDEIKIELPTQLHEKHHLLLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVT
gi 7513980	-----
gi 8923210	-----
	250 260 270 280 290 300

NOV9	-----
gi 12657106	SEQHIPVSANLPSGYLGYPELGMGRHYGPEIKWVDGKGKPLLKISTHLVSTVYTQDQHLHN
gi 5689453	SEQHIPVSANLPSGYLGYPELGMGRHYGPEIKWVDGKGKPLLKISTHLVSTVYTQDQHLHN
gi 7513980	-----
gi 8923210	-----
	310 320 330 340 350 360

NOV9	-----
gi 12657106	FFQYCQKTESGAQALGNELVKYLSLHAMEGHVMI AFLPTILNQLFRVLTRATQEEVAVN
gi 5689453	FFQYCQKTESGAQALGNELVKYLSLHAMEGHVMI AFLPTILNQLFRVLTRATQEEVAVN
gi 7513980	-----
gi 8923210	-----
	370 380 390 400 410 420

NOV9	-----
gi 12657106	VTRVIIHVVAQCHEEGLESHLRSYVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADF
gi 5689453	VTRVIIHVVAQCHEEGLESHLRSYVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADF
gi 7513980	-----
gi 8923210	-----
	430 440 450 460 470 480

NOV9	-----
gi 12657106	LTSNKLLKYSWFFFDVLIK SMAQH LIENSKVKLLRNQRF PASYHHAVETVVNMLMPHITQ
gi 5689453	LTSNKLLKYSWFFFDVLIK SMAQH LIENSKVKLLRNQRF PASYHHAVETVVNMLMPHITQ
gi 7513980	-----
gi 8923210	-----
	490 500 510 520 530 540

NOV9	-----
gi 12657106	KFRDNPEASKNANHSLAVFIKRCFTFMDRGFVFKQINNYISCFAPGDPKTLFEYKFEFLR
gi 5689453	KFRDNPEASKNANHSLAVFIKRCFTFMDRGFVFKQINNYISCFAPGDPKTLFEYKFEFLR
gi 7513980	-----
gi 8923210	-----
	550 560 570 580 590 600

NOV9	-----
gi 12657106	VVCNHEHYIPLNLPMPFGKGRIQRYQDLQLDYSLTDEF CRNHFLVGLLLREVGTALQEFR

gi 5689453	VVCNHEHYIPLNLPMPFGKGRIQRYQDLQLDYSLTDEFRCRNHFLVGLLLRVGTALQEFR
gi 7513980	-----
gi 8923210	-----
	610 620 630 640 650 660

NOV9	-----
gi 12657106	EVRLIAISVLKNLLIKHSFDDRYASRSHQARIATLYLPLFGLLIENVQRINVRDVSPPFV
gi 5689453	EVRLIAISVLKNLLIKHSFDDRYASRSHQARIATLYLPLFGLLIENVQRINVRDVSPPFV
gi 7513980	-----
gi 8923210	-----
	670 680 690 700 710 720

NOV9	-----
gi 12657106	NAGMTVKDESLALPAVNPLVTPQKGSTLDNSLHKDLLGAISGIASPYTTSTPNINSVRNA
gi 5689453	NAGMTVKDESLALPAVNPLVTPQKGSTLDNSLHKDLLGAISGIASPYTTSTPNINSVRNA
gi 7513980	-----
gi 8923210	-----
	730 740 750 760 770 780

NOV9	-----
gi 12657106	DSRGSLLISTDSGNSLPERNSEKSNLSDKHQSSSTLGNSVVRCDKLDQSEIKSLMCFLYI
gi 5689453	DSRGSLLISTDSGNSLPERNSEKSNLSDKHQSSSTLGNSVVRCDKLDQSEIKSLMCFLYI
gi 7513980	-----
gi 8923210	-----
	790 800 810 820 830 840

NOV9	-----
gi 12657106	LKSMSDDALFTYWNKASTSELMDFFTISEVCLHQFYMGKRYIARTGMMHARLQQLGSLD
gi 5689453	LKSMSDDALFTYWNKASTSELMDFFTISEVCLHQFYMGKRYIARTGMMHARLQQLGSLD
gi 7513980	-----
gi 8923210	-----
	850 860 870 880 890 900

NOV9	-----
gi 12657106	NSLTFNHSYGHSDADVLHQSLLEANIATEVCLTALDTLSLFTLAFKNQLLADHGHNPLMK
gi 5689453	NSLTFNHSYGHSDADVLHQSLLEANIATEVCLTALDTLSLFTLAFKNQLLADHGHNPLMK
gi 7513980	-----KLSRGHSPLMK
gi 8923210	-----
	910 920 930 940 950 960

NOV9	-----
gi 12657106	KVFDVYLCFLQKHQSEETALKNVFTALRS LIYKFPSTFYEGRADMCALCYEILKCCNSKL
gi 5689453	KVFDVYLCFLQKHQSEETALKNVFTALRS LIYKFPSTFYEGRADMCALCYEILKCCNSKL

gi 7513980	KVFDVYLCLFLOKHQSEMA	ALKNVFTALRS	LIYKFPSTFYEG	RADMCAS	LCYEVLKCCNSKL
gi 8923210	-----	-----	-----	-----	-----
	970	980	990	1000	1010 1020
				
NOV9	-----	-----	-----	-----	-----
gi 12657106	SSIRTEASQLLYFLMRNNFDY	TGKKSFVRTHLQVIIS	V	SQLIADVVGIGGTRFQ	QSLSI
gi 5689453	SSIRTEASQLLYFLMRNNFDY	TGKKSFVRTHLQVIIS	V	SQLIADVVGIGGTRFQ	QSLSI
gi 7513980	SSIRTEASQLLYFLMRNNFDY	TGKKSFVRTHLQVIIS	V	SQLIADVVGIGGTRFQ	QSLSI
gi 8923210	-----	-----	-----	-----	-----
	1030	1040	1050	1060	1070 1080
				
NOV9	-----	-----	-----	-----	-----
gi 12657106	-----	MKATAFPTEV	KDLTKRIC	TVLMATAQMKEHEK	DPPEMLTDLQCSLAKSYASI
gi 5689453	-----	MKATAFPTEV	KDLTKRIC	TVLMATAQMKEHEK	DPPEMLTDLQCSLAKSYAST
gi 7513980	-----	MKATAFPTEV	KDLTKRIC	TVLMATAQMKEHEK	DPPEMLTDLQCSLAKSYAST
gi 8923210	-----	MKATAFPTEV	KDLTKRIC	TVLMATAQMKEHEK	DPPEMLTDLQCSLAKSYAST
	1090	1100	1110	1120	1130 1140
				
NOV9	-----	-----	-----	-----	-----
gi 12657106	PELRKTWLDSMANIHVKN	GDSEAAMCYVHAAALVAE	ETIKSTYWK	-----	TQKILGTCL
gi 5689453	PELRKTWLDSMANIHVKN	GDSEAAMCYVHAAALVAE	ETIKSTYWK	-----	VQWEPP
gi 7513980	PELRKTWLDSMANIHVKN	GDSEAAMCYVHAAALVAE	ETIKSTYWK	-----	VQWEPP
gi 8923210	PELRKTWLDSMANIHVKN	GDSEAAMCYVHAAALVAE	ETIKSTYWK	-----	LAIGREPP
	1150	1160	1170	1180	1190 1200
				
NOV9	-----	-----	-----	-----	-----
gi 12657106	YHPCSSSSCRVSLK	KKKTPNGCSP	KKK	ITPNIIVEEGAVKED	AGMMDVHYSEVLELLEQ
gi 5689453	YHPCSSSSCRVSLK	KKKTPNGCSP	KKK	ITPNIIVEEGAVKED	AGMMDVHYSEVLELLEQ
gi 7513980	YHPCSSSSCRVSLK	KKKTPNGCSP	KKK	ITPNIIVEEGAVKED	AGMMDVHYSEVLELLEQ
gi 8923210	YHPCSSSSCRVSLK	KKKTPNGCSP	KKK	ITPNIIVEEGAVKED	AGMMDVHYSEVLELLEQ
	1210	1220	1230	1240	1250 1260
				
NOV9	-----	-----	-----	-----	-----
gi 12657106	CADGLWKAERYELIADI	VKLIPIYEKRRD	FEFLAHLYDTLH	RAYSKVTEVMHSGRRLLG	
gi 5689453	CADGLWKAERYELIADI	VKLIPIYEKRRD	FEFLAHLYDTLH	RAYSKVTEVMHSGRRLLG	
gi 7513980	CADGLWKAERYELIADI	VKLIPIYEKRRD	FEFLAHLYDTLH	RAYSKVTEVMHSGRRLLG	
gi 8923210	CADGLWKAERYELIADI	VKLIPIYEKRRD	FEFLAHLYDTLH	RAYSKVTEVMHSGRRLLG	
	1270	1280	1290	1300	1310 1320
				
NOV9	-----	-----	-----	-----	-----
gi 12657106	TYFRVAFFGC	AAQYQFTD	SETDVG	GFFFEDEDGKEYIYKEPKLTPLSEISQRLKLKLYSDKF	
gi 5689453	TYFRVAFFGC	AAQYQFTD	SETDVG	GFFFEDEDGKEYIYKEPKLTPLSEISQRLKLKLYSDKF	
gi 7513980	TYFRVAFFGC	AAQYQFTD	SETDVG	GFFFEDEDGKEYIYKEPKLTPLSEISQRLKLKLYSDKF	

gi 8923210	-----KRLFGRYRVAFYGGQGFEEEGKEYIYKEPKLTGLSEISORLLKLYADKF
	1330 1340 1350 1360 1370 1380
NOV9
gi 12657106	GMANVKKIQDIDEVNTKEFDPKYAHIQVTYVRFYFDKELTERKTEFCENHNTSRFVFEA
gi 5689453	GSENVKMIQDSGKVNPKDLDISKYAYIQVTHVTPFFDEKELQERKTEFERSHNIRRFMFEM
gi 7513980	GSENVKMIQDSGKVNPKDLDISKYAYIQVTHVTPFFDEKELQERKTEFERSHNIRRFMFEM
gi 8923210	GADNVKTIQDSNKNVPKDLDPKYAYIQVTYVTPFFDEKEIEDRHSDFEMHHNINRFVFEET
	1390 1400 1410 1420 1430 1440
NOV9
gi 12657106	PYTLSGKKQGCTEEQCKCRTILTTSKSFPYVRRRIPENCEQQINLKPTDVADEIKDKTA
gi 5689453	PFTQTGKROGGVEEQCKRRRTILTAIHCFPYVKKRIPVMYQHHTDLNPIEVAIDEMSKKVA
gi 7513980	PFTQTGKROGGVEEQCKRRRTILTAIHCFPYVKKRIPVMYQHHTDLNPIEVAIDEMSKKVA
gi 8923210	PFTLSGKKKHGGVAEQCKRRRTILTTSHLFPYVKKRIOVTSQSSTELNPIEVAIDEMSKKVS
	1450 1460 1470 1480 1490 1500
NOV9
gi 12657106	DLOKLCSSVYVDMITLQKLOGCVSMQVNAGPLAYAGAFINDSQASKYPRKVSSELKDMF
gi 5689453	EIRQLCSSAEVDMIKLQKLOGSVSVQVNAGPLAYARAFDDTNTKRYPDNKVKLLKEVF
gi 7513980	EIRQLCSSAEVDMIKLQKLOGSVSVQVNAGPLAYARAFDDTNTKRYPDNKVKLLKEVF
gi 8923210	EINQLCTMBEVDMITLQKLOGSVSVQVNAGPLAYARAFDEETNAKKYPDNQVKLLKEIF
	1510 1520 1530 1540 1550 1560
NOV9
gi 12657106	RKSTGACSIALELNEWLIKEDQLEYHEGLKSNFRDVF-----
gi 5689453	ROFVEACGOALAVNERLIKEDQLEYOEEMKANYREMAKELSEIMHEOLG-----
gi 7513980	ROFVEACGOALAVNERLIKEDQLEYOEEMKANYREIRKELSDIIVPRICPGEDKRATKFP
gi 8923210	ROFADACGOALAVNERLIKEDQLEYOEELRSTTFCTCSANSPQS-----
	1570 1580 1590 1600 1610 1620
NOV9
gi 12657106	-----
gi 5689453	-----
gi 7513980	AHLQRHQRTDNKHSGSRVDQFILSCVTLPHPEPHVGTCTCFVMCKLRRTTFRANHWFCAQEEA
gi 8923210	-----
	1630 1640
NOV9
gi 12657106	-----
gi 5689453	-----
gi 751380	MGNGREKEPWTVIFNSRFYRSWGKVHIFF
gi 8923210	-----

Other BLAST results include sequences from the Patp database, which is a proprietary database that contains sequences published in patents and patent publications. Patp results include those listed in Table 9E.

5

Table 9E. Patp alignments of NOV9			
Sequences producing High-scoring Segment Pairs:			Smallest
	Reading	High	Sum
	Frame	Score	Prob. P (N)
Patp:AAB64378 Amino acid sequence of human intracellular signaling, <i>Homo sapiens</i> , 747 aa	+1	1634	1.2e-208

For example, a BLAST against patp:AAB64378, a 747 amino acid human intracellular signaling molecule (INTRA10) (WO00/77040) from *Homo sapiens*, produced good identity, $E = 1.2e-208$.

As noted, the disclosed NOV9 protein showed good identity with a human intracellular signaling molecule. (See WO00/77040). Such intracellular signaling molecules may be useful for the diagnosis, prevention, and treatment of cell proliferative, autoimmune, inflammatory, neurological, gastrointestinal, reproductive, and developmental disorders. Modulators of the intracellular signaling molecules exhibit immunosuppressive, cytostatic, neuroprotective, nootropic, antiarteriosclerotic, anti-inflammatory, anti-HIV, neuroleptic, antibacterial, antifungal, antiviral, antiparasitic, antihelminthic, and antiparkinsonian activity. Disorders associated with abnormal intracellular signaling molecule expression or activity include cell proliferative disorders, e.g., arteriosclerosis and cancers; autoimmune or inflammatory disorders, e.g., Addison's disease and AIDS; viral, bacterial, fungal, parasitic, protozoal, and helminthic infections; gastrointestinal disorders, e.g. dysphagia and irritable bowel syndrome; neurological disorders, e.g., epilepsy and Parkinson's disease; and prion diseases, e.g., Creutzfeldt-Jakob disease and mental disorders, e.g., anxiety, schizophrenia and Tourette's disorder.

The pattern of expression of this gene and its family members, and its similarity to the TRG family of genes suggests that it may function as a TRG family protein. Therefore, the novel nucleic acids and proteins identified here may be useful in potential therapeutic applications implicated in (but not limited to) various pathologies and disorders as indicated

below. The potential therapeutic applications for this invention include, but are not limited to: protein therapeutic, small molecule drug target, antibody target (therapeutic, diagnostic, drug targeting/cytotoxic antibody), diagnostic and/or prognostic marker, gene therapy (gene delivery/gene ablation), research tools, tissue regeneration *in vivo* and *in vitro* of all tissues and cell types composing (but not limited to) those defined here.

The nucleic acids and proteins of the invention are useful in potential therapeutic applications implicated in hypo- and hyperthyroidism, disorders of the thyroid, cancer including but not limited to thyroid-related cancers, and/or other pathologies and disorders. For example, a cDNA encoding the TRG-like protein may be useful in gene therapy, and the TRG-like protein may be useful when administered to a subject in need thereof. By way of nonlimiting example, the compositions of the present invention will have efficacy for treatment of patients suffering from hypo- and hyperthyroidism, disorders of the thyroid, cancer including but not limited to thyroid-related cancers. The novel nucleic acid encoding TRG-like protein, and the TRG-like protein of the invention, or fragments thereof, may further be useful in diagnostic applications, wherein the presence or amount of the nucleic acid or the protein are to be assessed. These materials are further useful in the generation of antibodies that bind immunospecifically to the novel substances of the invention for use in therapeutic or diagnostic methods.

These materials are further useful in the generation of antibodies that bind immunospecifically to the novel NOV9 substances for use in therapeutic or diagnostic methods. These antibodies may be generated according to methods known in the art, using prediction from hydrophobicity charts, as described in the "Anti-NOVX Antibodies" section below.

NOVX Nucleic Acids and Polypeptides

One aspect of the invention pertains to isolated nucleic acid molecules that encode NOVX polypeptides or biologically active portions thereof. Also included in the invention are nucleic acid fragments sufficient for use as hybridization probes to identify NOVX-encoding nucleic acids (*e.g.*, NOVX mRNAs) and fragments for use as PCR primers for the amplification and/or mutation of NOVX nucleic acid molecules. As used herein, the term "nucleic acid molecule" is intended to include DNA molecules (*e.g.*, cDNA or genomic DNA), RNA molecules (*e.g.*, mRNA), analogs of the DNA or RNA generated using nucleotide analogs, and

derivatives, fragments and homologs thereof. The nucleic acid molecule may be single-stranded or double-stranded, but preferably is comprised double-stranded DNA.

An NOVX nucleic acid can encode a mature NOVX polypeptide. As used herein, a “mature” form of a polypeptide or protein disclosed in the present invention is the product of a naturally occurring polypeptide or precursor form or proprotein. The naturally occurring polypeptide, precursor or proprotein includes, by way of nonlimiting example, the full-length gene product, encoded by the corresponding gene. Alternatively, it may be defined as the polypeptide, precursor or proprotein encoded by an ORF described herein. The product “mature” form arises, again by way of nonlimiting example, as a result of one or more naturally occurring processing steps as they may take place within the cell, or host cell, in which the gene product arises. Examples of such processing steps leading to a “mature” form of a polypeptide or protein include the cleavage of the N-terminal methionine residue encoded by the initiation codon of an ORF, or the proteolytic cleavage of a signal peptide or leader sequence. Thus a mature form arising from a precursor polypeptide or protein that has residues 1 to N, where residue 1 is the N-terminal methionine, would have residues 2 through N remaining after removal of the N-terminal methionine. Alternatively, a mature form arising from a precursor polypeptide or protein having residues 1 to N, in which an N-terminal signal sequence from residue 1 to residue M is cleaved, would have the residues from residue M+1 to residue N remaining. Further as used herein, a “mature” form of a polypeptide or protein may arise from a step of post-translational modification other than a proteolytic cleavage event. Such additional processes include, by way of non-limiting example, glycosylation, myristoylation or phosphorylation. In general, a mature polypeptide or protein may result from the operation of only one of these processes, or a combination of any of them.

The term “probes”, as utilized herein, refers to nucleic acid sequences of variable length, preferably between at least about 10 nucleotides (nt), 100 nt, or as many as approximately, *e.g.*, 6,000 nt, depending upon the specific use. Probes are used in the detection of identical, similar, or complementary nucleic acid sequences. Longer length probes are generally obtained from a natural or recombinant source, are highly specific, and much slower to hybridize than shorter-length oligomer probes. Probes may be single- or double-stranded and designed to have specificity in PCR, membrane-based hybridization technologies, or ELISA-like technologies.

The term “isolated” nucleic acid molecule, as utilized herein, is one, which is separated from other nucleic acid molecules which are present in the natural source of the nucleic acid.

Preferably, an "isolated" nucleic acid is free of sequences which naturally flank the nucleic acid (*i.e.*, sequences located at the 5'- and 3'-termini of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated NOVX nucleic acid molecules can contain less than about 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb or 0.1 kb of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell/tissue from which the nucleic acid is derived (*e.g.*, brain, heart, liver, spleen, etc.). Moreover, an "isolated" nucleic acid molecule, such as a cDNA molecule, can be substantially free of other cellular material or culture medium when produced by recombinant techniques, or of chemical precursors or other chemicals when chemically synthesized.

A nucleic acid molecule of the invention, *e.g.*, a nucleic acid molecule having the nucleotide sequence SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, or 33, or a complement of this aforementioned nucleotide sequence, can be isolated using standard molecular biology techniques and the sequence information provided herein. Using all or a portion of the nucleic acid sequence of SEQ ID NOS 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, or 33 as a hybridization probe, NOVX molecules can be isolated using standard hybridization and cloning techniques (*e.g.*, as described in Sambrook, *et al.*, (eds.), MOLECULAR CLONING: A LABORATORY MANUAL 2nd Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989; and Ausubel, *et al.*, (eds.), CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, New York, NY, 1993.)

A nucleic acid of the invention can be amplified using cDNA, mRNA or alternatively, genomic DNA, as a template and appropriate oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding to NOVX nucleotide sequences can be prepared by standard synthetic techniques, *e.g.*, using an automated DNA synthesizer.

As used herein, the term "oligonucleotide" refers to a series of linked nucleotide residues, which oligonucleotide has a sufficient number of nucleotide bases to be used in a PCR reaction. A short oligonucleotide sequence may be based on, or designed from, a genomic or cDNA sequence and is used to amplify, confirm, or reveal the presence of an identical, similar or complementary DNA or RNA in a particular cell or tissue. Oligonucleotides comprise portions of a nucleic acid sequence having about 10 nt, 50 nt, or 100 nt in length, preferably about 15 nt to 30 nt in length. In one embodiment of the invention, an oligonucleotide

comprising a nucleic acid molecule less than 100 nt in length would further comprise at least 6 contiguous nucleotides SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, and 33, or a complement thereof. Oligonucleotides may be chemically synthesized and may also be used as probes.

5 In another embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule that is a complement of the nucleotide sequence shown in SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, or 33, or a portion of this nucleotide sequence (*e.g.*, a fragment that can be used as a probe or primer or a fragment encoding a biologically-active portion of an NOVX polypeptide). A nucleic acid molecule that is
10 complementary to the nucleotide sequence shown SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, or 33 is one that is sufficiently complementary to the nucleotide sequence shown SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, or 33 that it can hydrogen bond with little or no mismatches to the nucleotide sequence shown SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, or 33, thereby forming a stable duplex.

15 As used herein, the term “complementary” refers to Watson-Crick or Hoogsteen base pairing between nucleotides units of a nucleic acid molecule, and the term “binding” means the physical or chemical interaction between two polypeptides or compounds or associated polypeptides or compounds or combinations thereof. Binding includes ionic, non-ionic, van der Waals, hydrophobic interactions, and the like. A physical interaction can be either direct or
20 indirect. Indirect interactions may be through or due to the effects of another polypeptide or compound. Direct binding refers to interactions that do not take place through, or due to, the effect of another polypeptide or compound, but instead are without other substantial chemical intermediates.

Fragments provided herein are defined as sequences of at least 6 (contiguous) nucleic
25 acids or at least 4 (contiguous) amino acids, a length sufficient to allow for specific hybridization in the case of nucleic acids or for specific recognition of an epitope in the case of amino acids, respectively, and are at most some portion less than a full length sequence. Fragments may be derived from any contiguous portion of a nucleic acid or amino acid sequence of choice. Derivatives are nucleic acid sequences or amino acid sequences formed
30 from the native compounds either directly or by modification or partial substitution. Analogs are nucleic acid sequences or amino acid sequences that have a structure similar to, but not identical to, the native compound but differs from it in respect to certain components or side

chains. Analogs may be synthetic or from a different evolutionary origin and may have a similar or opposite metabolic activity compared to wild type. Homologs are nucleic acid sequences or amino acid sequences of a particular gene that are derived from different species.

Derivatives and analogs may be full length or other than full length, if the derivative or analog contains a modified nucleic acid or amino acid, as described below. Derivatives or analogs of the nucleic acids or proteins of the invention include, but are not limited to, molecules comprising regions that are substantially homologous to the nucleic acids or proteins of the invention, in various embodiments, by at least about 70%, 80%, or 95% identity (with a preferred identity of 80-95%) over a nucleic acid or amino acid sequence of identical size or when compared to an aligned sequence in which the alignment is done by a computer homology program known in the art, or whose encoding nucleic acid is capable of hybridizing to the complement of a sequence encoding the aforementioned proteins under stringent, moderately stringent, or low stringent conditions. *See e.g.* Ausubel, *et al.*, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, New York, NY, 1993, and below.

A “homologous nucleic acid sequence” or “homologous amino acid sequence,” or variations thereof, refer to sequences characterized by a homology at the nucleotide level or amino acid level as discussed above. Homologous nucleotide sequences encode those sequences coding for isoforms of NOVX polypeptides. Isoforms can be expressed in different tissues of the same organism as a result of, for example, alternative splicing of RNA.

Alternatively, isoforms can be encoded by different genes. In the invention, homologous nucleotide sequences include nucleotide sequences encoding for an NOVX polypeptide of species other than humans, including, but not limited to: vertebrates, and thus can include, *e.g.*, frog, mouse, rat, rabbit, dog, cat, cow, horse, and other organisms. Homologous nucleotide sequences also include, but are not limited to, naturally occurring allelic variations and mutations of the nucleotide sequences set forth herein. A homologous nucleotide sequence does not, however, include the exact nucleotide sequence encoding human NOVX protein. Homologous nucleic acid sequences include those nucleic acid sequences that encode conservative amino acid substitutions (see below) in SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, or 33, as well as a polypeptide possessing NOVX biological activity. Various biological activities of the NOVX proteins are described below.

An NOVX polypeptide is encoded by the open reading frame (“ORF”) of an NOVX nucleic acid. An ORF corresponds to a nucleotide sequence that could potentially be translated

into a polypeptide. A stretch of nucleic acids comprising an ORF is uninterrupted by a stop codon. An ORF that represents the coding sequence for a full protein begins with an ATG "start" codon and terminates with one of the three "stop" codons, namely, TAA, TAG, or TGA. For the purposes of this invention, an ORF may be any part of a coding sequence, with or
5 without a start codon, a stop codon, or both. For an ORF to be considered as a good candidate for coding for a *bona fide* cellular protein, a minimum size requirement is often set, *e.g.*, a stretch of DNA that would encode a protein of 50 amino acids or more.

The nucleotide sequences determined from the cloning of the human NOVX genes allows for the generation of probes and primers designed for use in identifying and/or cloning
10 NOVX homologues in other cell types, *e.g.* from other tissues, as well as NOVX homologues from other vertebrates. The probe/primer typically comprises substantially purified oligonucleotide. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 12, 25, 50, 100, 150, 200, 250, 300, 350 or 400 consecutive sense strand nucleotide sequence SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17,
15 19, 21, 23, 25, 27, 29, 31, or 33; or an anti-sense strand nucleotide sequence of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, or 33; or of a naturally occurring mutant of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, or 33.

Probes based on the human NOVX nucleotide sequences can be used to detect transcripts or genomic sequences encoding the same or homologous proteins. In various
20 embodiments, the probe further comprises a label group attached thereto, *e.g.* the label group can be a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be used as a part of a diagnostic test kit for identifying cells or tissues which mis-express an NOVX protein, such as by measuring a level of an NOVX-encoding nucleic acid in a sample of cells from a subject *e.g.*, detecting NOVX mRNA levels or determining whether a
25 genomic NOVX gene has been mutated or deleted.

"A polypeptide having a biologically-active portion of an NOVX polypeptide" refers to polypeptides exhibiting activity similar, but not necessarily identical to, an activity of a polypeptide of the invention, including mature forms, as measured in a particular biological assay, with or without dose dependency. A nucleic acid fragment encoding a "biologically-
30 active portion of NOVX" can be prepared by isolating a portion SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, or 33, that encodes a polypeptide having an NOVX biological activity (the biological activities of the NOVX proteins are described below),

expressing the encoded portion of NOVX protein (*e.g.*, by recombinant expression *in vitro*) and assessing the activity of the encoded portion of NOVX.

NOVX Nucleic Acid and Polypeptide Variants

The invention further encompasses nucleic acid molecules that differ from the nucleotide sequences shown in SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, or 33 due to degeneracy of the genetic code and thus encode the same NOVX proteins as that encoded by the nucleotide sequences shown in SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, or 33. In another embodiment, an isolated nucleic acid molecule of the invention has a nucleotide sequence encoding a protein having an amino acid sequence shown in SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, or 34.

In addition to the human NOVX nucleotide sequences shown in SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, or 33, it will be appreciated by those skilled in the art that DNA sequence polymorphisms that lead to changes in the amino acid sequences of the NOVX polypeptides may exist within a population (*e.g.*, the human population). Such genetic polymorphism in the NOVX genes may exist among individuals within a population due to natural allelic variation. As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame (ORF) encoding an NOVX protein, preferably a vertebrate NOVX protein. Such natural allelic variations can typically result in 1-5% variance in the nucleotide sequence of the NOVX genes. Any and all such nucleotide variations and resulting amino acid polymorphisms in the NOVX polypeptides, which are the result of natural allelic variation and that do not alter the functional activity of the NOVX polypeptides, are intended to be within the scope of the invention.

Moreover, nucleic acid molecules encoding NOVX proteins from other species, and thus that have a nucleotide sequence that differs from the human SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, or 33 are intended to be within the scope of the invention. Nucleic acid molecules corresponding to natural allelic variants and homologues of the NOVX cDNAs of the invention can be isolated based on their homology to the human NOVX nucleic acids disclosed herein using the human cDNAs, or a portion thereof, as a hybridization probe according to standard hybridization techniques under stringent hybridization conditions.

Accordingly, in another embodiment, an isolated nucleic acid molecule of the invention is at least 6 nucleotides in length and hybridizes under stringent conditions to the nucleic acid

molecule comprising the nucleotide sequence of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, or 33. In another embodiment, the nucleic acid is at least 10, 25, 50, 100, 250, 500, 750, 1000, 1500, or 2000 or more nucleotides in length. In yet another embodiment, an isolated nucleic acid molecule of the invention hybridizes to the coding region. As used
5 herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 60% homologous to each other typically remain hybridized to each other.

Homologs (*i.e.*, nucleic acids encoding NOVX proteins derived from species other than human) or other related sequences (*e.g.*, paralogs) can be obtained by low, moderate or high
10 stringency hybridization with all or a portion of the particular human sequence as a probe using methods well known in the art for nucleic acid hybridization and cloning.

As used herein, the phrase "stringent hybridization conditions" refers to conditions under which a probe, primer or oligonucleotide will hybridize to its target sequence, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different
15 circumstances. Longer sequences hybridize specifically at higher temperatures than shorter sequences. Generally, stringent conditions are selected to be about 5 °C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength, pH and nucleic acid concentration) at which 50% of the probes complementary to the target sequence hybridize to the target sequence at
20 equilibrium. Since the target sequences are generally present at excess, at T_m, 50% of the probes are occupied at equilibrium. Typically, stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion (or other salts) at
pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes, primers or
25 oligonucleotides (*e.g.*, 10 nt to 50 nt) and at least about 60°C for longer probes, primers and oligonucleotides. Stringent conditions may also be achieved with the addition of destabilizing agents, such as formamide.

Stringent conditions are known to those skilled in the art and can be found in Ausubel, *et al.*, (eds.), CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, N.Y. (1989),
30 6.3.1-6.3.6. Preferably, the conditions are such that sequences at least about 65%, 70%, 75%, 85%, 90%, 95%, 98%, or 99% homologous to each other typically remain hybridized to each other. A non-limiting example of stringent hybridization conditions are hybridization in a high

salt buffer comprising 6X SSC, 50 mM Tris-HCl (pH 7.5), 1 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.02% BSA, and 500 mg/ml denatured salmon sperm DNA at 65°C, followed by one or more washes in 0.2X SSC, 0.01% BSA at 50°C. An isolated nucleic acid molecule of the invention that hybridizes under stringent conditions to the sequences SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, or 33, corresponds to a naturally-occurring nucleic acid molecule. As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (*e.g.*, encodes a natural protein).

In a second embodiment, a nucleic acid sequence that is hybridizable to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, or 33, or fragments, analogs or derivatives thereof, under conditions of moderate stringency is provided. A non-limiting example of moderate stringency hybridization conditions are hybridization in 6X SSC, 5X Denhardt's solution, 0.5% SDS and 100 mg/ml denatured salmon sperm DNA at 55°C, followed by one or more washes in 1X SSC, 0.1% SDS at 37°C. Other conditions of moderate stringency that may be used are well-known within the art. *See, e.g.*, Ausubel, *et al.* (eds.), 1993, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, NY, and Kriegler, 1990; GENE TRANSFER AND EXPRESSION, A LABORATORY MANUAL, Stockton Press, NY.

In a third embodiment, a nucleic acid that is hybridizable to the nucleic acid molecule comprising the nucleotide sequences SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, or 33, or fragments, analogs or derivatives thereof, under conditions of low stringency, is provided. A non-limiting example of low stringency hybridization conditions are hybridization in 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 mg/ml denatured salmon sperm DNA, 10% (wt/vol) dextran sulfate at 40°C, followed by one or more washes in 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS at 50°C. Other conditions of low stringency that may be used are well known in the art (*e.g.*, as employed for cross-species hybridizations). *See, e.g.*, Ausubel, *et al.* (eds.), 1993, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, NY, and Kriegler, 1990, GENE TRANSFER AND EXPRESSION, A LABORATORY MANUAL, Stockton Press, NY; Shilo and Weinberg, 1981. *Proc Natl Acad Sci USA* 78: 6789-6792.

Conservative Mutations

In addition to naturally-occurring allelic variants of NOVX sequences that may exist in the population, the skilled artisan will further appreciate that changes can be introduced by mutation into the nucleotide sequences SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, or 33, thereby leading to changes in the amino acid sequences of the encoded NOVX proteins, without altering the functional ability of said NOVX proteins. For example, nucleotide substitutions leading to amino acid substitutions at "non-essential" amino acid residues can be made in the sequence SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, or 34. A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequences of the NOVX proteins without altering their biological activity, whereas an "essential" amino acid residue is required for such biological activity. For example, amino acid residues that are conserved among the NOVX proteins of the invention are predicted to be particularly non-amenable to alteration. Amino acids for which conservative substitutions can be made are well-known within the art.

Another aspect of the invention pertains to nucleic acid molecules encoding NOVX proteins that contain changes in amino acid residues that are not essential for activity. Such NOVX proteins differ in amino acid sequence from SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, or 33 yet retain biological activity. In one embodiment, the isolated nucleic acid molecule comprises a nucleotide sequence encoding a protein, wherein the protein comprises an amino acid sequence at least about 45% homologous to the amino acid sequences SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, and 34. Preferably, the protein encoded by the nucleic acid molecule is at least about 60% homologous to SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, and 34; more preferably at least about 70% homologous SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, or 34; still more preferably at least about 80% homologous to SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, or 34; even more preferably at least about 90% homologous to SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, or 34; and most preferably at least about 95% homologous to SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, or 34.

An isolated nucleic acid molecule encoding an NOVX protein homologous to the protein of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, or 34 can be created by introducing one or more nucleotide substitutions, additions or deletions into the

nucleotide sequence of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, or 33, such that one or more amino acid substitutions, additions or deletions are introduced into the encoded protein.

Mutations can be introduced into SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, or 33 by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted, non-essential amino acid residues. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined within the art. These families include amino acids with basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.*, aspartic acid, glutamic acid), uncharged polar side chains (*e.g.*, glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (*e.g.*, alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (*e.g.*, threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted non-essential amino acid residue in the NOVX protein is replaced with another amino acid residue from the same side chain family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of an NOVX coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for NOVX biological activity to identify mutants that retain activity. Following mutagenesis SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, or 33, the encoded protein can be expressed by any recombinant technology known in the art and the activity of the protein can be determined.

The relatedness of amino acid families may also be determined based on side chain interactions. Substituted amino acids may be fully conserved "strong" residues or fully conserved "weak" residues. The "strong" group of conserved amino acid residues may be any one of the following groups: STA, NEQK, NHQK, NDEQ, QHRK, MILV, MILF, HY, FYW, wherein the single letter amino acid codes are grouped by those amino acids that may be substituted for each other. Likewise, the "weak" group of conserved residues may be any one of the following: CSA, ATV, SAG, STNK, STPA, SGND, SNDEQK, NDEQHK, NEQHRK, VLIM, HFY, wherein the letters within each group represent the single letter amino acid code.

In one embodiment, a mutant NOVX protein can be assayed for (i) the ability to form protein:protein interactions with other NOVX proteins, other cell-surface proteins, or

biologically-active portions thereof, (ii) complex formation between a mutant NOVX protein and an NOVX ligand; or (iii) the ability of a mutant NOVX protein to bind to an intracellular target protein or biologically-active portion thereof; (e.g. avidin proteins).

In yet another embodiment, a mutant NOVX protein can be assayed for the ability to regulate a specific biological function (e.g., regulation of insulin release).

Antisense Nucleic Acids

Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, or 33, or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein (e.g., complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence). In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, 25, 50, 100, 250 or 500 nucleotides or an entire NOVX coding strand, or to only a portion thereof. Nucleic acid molecules encoding fragments, homologs, derivatives and analogs of an NOVX protein of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, or 34, or antisense nucleic acids complementary to an NOVX nucleic acid sequence of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, or 33, are additionally provided.

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence encoding an NOVX protein. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues. In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence encoding the NOVX protein. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding the NOVX protein disclosed herein, antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of NOVX mRNA, but more preferably is an oligonucleotide that is

antisense to only a portion of the coding or noncoding region of NOVX mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of NOVX mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention
5 can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally-occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids (*e.g.*,
10 phosphorothioate derivatives and acridine substituted nucleotides can be used).

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine,
15 inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil,
20 queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the
25 inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a subject or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding an NOVX protein to thereby inhibit expression of the protein (*e.g.*, by
30 inhibiting transcription and/or translation). The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major

groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface (e.g., by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens). The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient nucleic acid molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α -anomeric nucleic acid molecule. An α -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β -units, the strands run parallel to each other. See, e.g., Gaultier, *et al.*, 1987. *Nucl. Acids Res.* **15**: 6625-6641. The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (See, e.g., Inoue, *et al.* 1987. *Nucl. Acids Res.* **15**: 6131-6148) or a chimeric RNA-DNA analogue (See, e.g., Inoue, *et al.*, 1987. *FEBS Lett.* **215**: 327-330).

Ribozymes and PNA Moieties

Nucleic acid modifications include, by way of non-limiting example, modified bases, and nucleic acids whose sugar phosphate backbones are modified or derivatized. These modifications are carried out at least in part to enhance the chemical stability of the modified nucleic acid, such that they may be used, for example, as antisense binding nucleic acids in therapeutic applications in a subject.

In one embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (e.g., hammerhead ribozymes as described in Haselhoff and Gerlach 1988. *Nature* 334: 585-591) can be used to catalytically cleave NOVX mRNA transcripts to thereby inhibit translation of NOVX mRNA. A ribozyme having specificity for an NOVX-encoding nucleic acid can be designed based upon the nucleotide sequence of an NOVX cDNA disclosed herein (i.e., SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, or 33). For

example, a derivative of a *Tetrahymena* L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in an NOVX-encoding mRNA. See, e.g., U.S. Patent 4,987,071 to Cech, *et al.* and U.S. Patent 5,116,742 to Cech, *et al.* NOVX mRNA can also be used to select a catalytic RNA
5 having a specific ribonuclease activity from a pool of RNA molecules. See, e.g., Bartel *et al.*, (1993) *Science* 261:1411-1418.

Alternatively, NOVX gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of the NOVX nucleic acid (e.g., the NOVX promoter and/or enhancers) to form triple helical structures that prevent transcription of the
10 NOVX gene in target cells. See, e.g., Helene, 1991. *Anticancer Drug Des.* 6: 569-84; Helene, *et al.* 1992. *Ann. N.Y. Acad. Sci.* 660: 27-36; Maher, 1992. *Bioassays* 14: 807-15.

In various embodiments, the NOVX nucleic acids can be modified at the base moiety, sugar moiety or phosphate backbone to improve, e.g., the stability, hybridization, or solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be
15 modified to generate peptide nucleic acids. See, e.g., Hyrup, *et al.*, 1996. *Bioorg Med Chem* 4: 5-23. As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics (e.g., DNA mimics) in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has been shown to allow for specific hybridization to DNA and RNA under
20 conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide synthesis protocols as described in Hyrup, *et al.*, 1996. *supra*; Perry-O'Keefe, *et al.*, 1996. *Proc. Natl. Acad. Sci. USA* 93: 14670-14675.

PNAs of NOVX can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene
25 expression by, e.g., inducing transcription or translation arrest or inhibiting replication. PNAs of NOVX can also be used, for example, in the analysis of single base pair mutations in a gene (e.g., PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, e.g., S₁ nucleases (See, Hyrup, *et al.*, 1996. *supra*); or as probes or primers for DNA sequence and hybridization (See, Hyrup, *et al.*, 1996, *supra*; Perry-O'Keefe, *et al.*,
30 1996. *supra*).

In another embodiment, PNAs of NOVX can be modified, e.g., to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of

PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras of NOVX can be generated that may combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes (e.g., RNase H and DNA polymerases) to interact with the DNA portion while the PNA portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (*see*, Hyrup, et al., 1996. *supra*). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup, *et al.*, 1996. *supra* and Finn, *et al.*, 1996. *Nucl Acids Res* 24: 3357-3363. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry, and modified nucleoside analogs, e.g., 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite, can be used between the PNA and the 5' end of DNA. *See*, e.g., Mag, *et al.*, 1989. *Nucl Acid Res* 17: 5973-5988. PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment. *See*, e.g., Finn, *et al.*, 1996. *supra*. Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment. *See*, e.g., Petersen, *et al.*, 1975. *Bioorg. Med. Chem. Lett.* 5: 1119-11124.

In other embodiments, the oligonucleotide may include other appended groups such as peptides (e.g., for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (*see*, e.g., Letsinger, *et al.*, 1989. *Proc. Natl. Acad. Sci. U.S.A.* 86: 6553-6556; Lemaitre, *et al.*, 1987. *Proc. Natl. Acad. Sci.* 84: 648-652; PCT Publication No. WO88/09810) or the blood-brain barrier (*see*, e.g., PCT Publication No. WO 89/10134). In addition, oligonucleotides can be modified with hybridization triggered cleavage agents (*see*, e.g., Krol, *et al.*, 1988. *BioTechniques* 6:958-976) or intercalating agents (*see*, e.g., Zon, 1988. *Pharm. Res.* 5: 539-549). To this end, the oligonucleotide may be conjugated to another molecule, e.g., a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, and the like.

NOVX Polypeptides

A polypeptide according to the invention includes a polypeptide including the amino acid sequence of NOVX polypeptides whose sequences are provided in SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, or 34. The invention also includes a mutant or variant protein any of whose residues may be changed from the corresponding residues shown

in SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, or 34 while still encoding a protein that maintains its NOVX activities and physiological functions, or a functional fragment thereof.

In general, an NOVX variant that preserves NOVX-like function includes any variant in which residues at a particular position in the sequence have been substituted by other amino acids, and further include the possibility of inserting an additional residue or residues between two residues of the parent protein as well as the possibility of deleting one or more residues from the parent sequence. Any amino acid substitution, insertion, or deletion is encompassed by the invention. In favorable circumstances, the substitution is a conservative substitution as defined above.

One aspect of the invention pertains to isolated NOVX proteins, and biologically-active portions thereof, or derivatives, fragments, analogs or homologs thereof. Also provided are polypeptide fragments suitable for use as immunogens to raise anti-NOVX antibodies. In one embodiment, native NOVX proteins can be isolated from cells or tissue sources by an appropriate purification scheme using standard protein purification techniques. In another embodiment, NOVX proteins are produced by recombinant DNA techniques. Alternative to recombinant expression, an NOVX protein or polypeptide can be synthesized chemically using standard peptide synthesis techniques.

An "isolated" or "purified" polypeptide or protein or biologically-active portion thereof is substantially free of cellular material or other contaminating proteins from the cell or tissue source from which the NOVX protein is derived, or substantially free from chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of NOVX proteins in which the protein is separated from cellular components of the cells from which it is isolated or recombinantly-produced. In one embodiment, the language "substantially free of cellular material" includes preparations of NOVX proteins having less than about 30% (by dry weight) of non-NOVX proteins (also referred to herein as a "contaminating protein"), more preferably less than about 20% of non-NOVX proteins, still more preferably less than about 10% of non-NOVX proteins, and most preferably less than about 5% of non-NOVX proteins. When the NOVX protein or biologically-active portion thereof is recombinantly-produced, it is also preferably substantially free of culture medium, *i.e.*, culture medium represents less than about 20%, more preferably

less than about 10%, and most preferably less than about 5% of the volume of the NOVX protein preparation.

The language "substantially free of chemical precursors or other chemicals" includes preparations of NOVX proteins in which the protein is separated from chemical precursors or other chemicals that are involved in the synthesis of the protein. In one embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of NOVX proteins having less than about 30% (by dry weight) of chemical precursors or non-NOVX chemicals, more preferably less than about 20% chemical precursors or non-NOVX chemicals, still more preferably less than about 10% chemical precursors or non-NOVX chemicals, and most preferably less than about 5% chemical precursors or non-NOVX chemicals.

Biologically-active portions of NOVX proteins include peptides comprising amino acid sequences sufficiently homologous to or derived from the amino acid sequences of the NOVX proteins (*e.g.*, the amino acid sequence shown in SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, or 34) that include fewer amino acids than the full-length NOVX proteins, and exhibit at least one activity of an NOVX protein. Typically, biologically-active portions comprise a domain or motif with at least one activity of the NOVX protein. A biologically-active portion of an NOVX protein can be a polypeptide which is, for example, 10, 25, 50, 100 or more amino acid residues in length.

Moreover, other biologically-active portions, in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the functional activities of a native NOVX protein.

In an embodiment, the NOVX protein has an amino acid sequence shown SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, or 34. In other embodiments, the NOVX protein is substantially homologous to SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, or 34, and retains the functional activity of the protein of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, or 34, yet differs in amino acid sequence due to natural allelic variation or mutagenesis, as described in detail, below. Accordingly, in another embodiment, the NOVX protein is a protein that comprises an amino acid sequence at least about 45% homologous to the amino acid sequence SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, or 34, and retains the functional activity of the NOVX proteins of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, or 34.

Determining Homology Between Two or More Sequences

To determine the percent homology of two amino acid sequences or of two nucleic acids, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in the sequence of a first amino acid or nucleic acid sequence for optimal alignment with a second amino or nucleic acid sequence). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in the first sequence is occupied by the same amino acid residue or nucleotide as the corresponding position in the second sequence, then the molecules are homologous at that position (*i.e.*, as used herein amino acid or nucleic acid "homology" is equivalent to amino acid or nucleic acid "identity").

The nucleic acid sequence homology may be determined as the degree of identity between two sequences. The homology may be determined using computer programs known in the art, such as GAP software provided in the GCG program package. *See*, Needleman and Wunsch, 1970. *J Mol Biol* 48: 443-453. Using GCG GAP software with the following settings for nucleic acid sequence comparison: GAP creation penalty of 5.0 and GAP extension penalty of 0.3, the coding region of the analogous nucleic acid sequences referred to above exhibits a degree of identity preferably of at least 70%, 75%, 80%, 85%, 90%, 95%, 98%, or 99%, with the CDS (encoding) part of the DNA sequence shown in SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, or 33.

The term "sequence identity" refers to the degree to which two polynucleotide or polypeptide sequences are identical on a residue-by-residue basis over a particular region of comparison. The term "percentage of sequence identity" is calculated by comparing two optimally aligned sequences over that region of comparison, determining the number of positions at which the identical nucleic acid base (*e.g.*, A, T, C, G, U, or I, in the case of nucleic acids) occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the region of comparison (*i.e.*, the window size), and multiplying the result by 100 to yield the percentage of sequence identity. The term "substantial identity" as used herein denotes a characteristic of a polynucleotide sequence, wherein the polynucleotide comprises a sequence that has at least 80 percent sequence identity, preferably at least 85 percent identity and often 90 to 95 percent sequence

identity, more usually at least 99 percent sequence identity as compared to a reference sequence over a comparison region.

Chimeric and Fusion Proteins

5 The invention also provides NOVX chimeric or fusion proteins. As used herein, an NOVX "chimeric protein" or "fusion protein" comprises an NOVX polypeptide operatively-linked to a non-NOVX polypeptide. An "NOVX polypeptide" refers to a polypeptide having an amino acid sequence corresponding to an NOVX protein SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, or 34), whereas a "non-NOVX polypeptide" refers to a
10 polypeptide having an amino acid sequence corresponding to a protein that is not substantially homologous to the NOVX protein, *e.g.*, a protein that is different from the NOVX protein and that is derived from the same or a different organism. Within an NOVX fusion protein the NOVX polypeptide can correspond to all or a portion of an NOVX protein. In one embodiment, an NOVX fusion protein comprises at least one biologically-active portion of an
15 NOVX protein. In another embodiment, an NOVX fusion protein comprises at least two biologically-active portions of an NOVX protein. In yet another embodiment, an NOVX fusion protein comprises at least three biologically-active portions of an NOVX protein. Within the fusion protein, the term "operatively-linked" is intended to indicate that the NOVX polypeptide and the non-NOVX polypeptide are fused in-frame with one another. The non-NOVX
20 polypeptide can be fused to the N-terminus or C-terminus of the NOVX polypeptide.

In one embodiment, the fusion protein is a GST-NOVX fusion protein in which the NOVX sequences are fused to the C-terminus of the GST (glutathione S-transferase) sequences. Such fusion proteins can facilitate the purification of recombinant NOVX polypeptides.

In another embodiment, the fusion protein is an NOVX protein containing a
25 heterologous signal sequence at its N-terminus. In certain host cells (*e.g.*, mammalian host cells), expression and/or secretion of NOVX can be increased through use of a heterologous signal sequence.

In yet another embodiment, the fusion protein is an NOVX-immunoglobulin fusion protein in which the NOVX sequences are fused to sequences derived from a member of the immunoglobulin protein family. The NOVX-immunoglobulin fusion proteins of the invention
30 can be incorporated into pharmaceutical compositions and administered to a subject to inhibit an interaction between an NOVX ligand and an NOVX protein on the surface of a cell, to

thereby suppress NOVX-mediated signal transduction *in vivo*. The NOVX-immunoglobulin fusion proteins can be used to affect the bioavailability of an NOVX cognate ligand. Inhibition of the NOVX ligand/NOVX interaction may be useful therapeutically for both the treatment of proliferative and differentiative disorders, as well as modulating (*e.g.* promoting or inhibiting) cell survival. Moreover, the NOVX-immunoglobulin fusion proteins of the invention can be used as immunogens to produce anti-NOVX antibodies in a subject, to purify NOVX ligands, and in screening assays to identify molecules that inhibit the interaction of NOVX with an NOVX ligand.

An NOVX chimeric or fusion protein of the invention can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, *e.g.*, by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that give rise to complementary overhangs between two consecutive gene fragments that can subsequently be annealed and reamplified to generate a chimeric gene sequence (*see, e.g.*, Ausubel, *et al.* (eds.) CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST polypeptide). An NOVX-encoding nucleic acid can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the NOVX protein.

NOVX Agonists and Antagonists

The invention also pertains to variants of the NOVX proteins that function as either NOVX agonists (*i.e.*, mimetics) or as NOVX antagonists. Variants of the NOVX protein can be generated by mutagenesis (*e.g.*, discrete point mutation or truncation of the NOVX protein). An agonist of the NOVX protein can retain substantially the same, or a subset of, the biological activities of the naturally occurring form of the NOVX protein. An antagonist of the NOVX protein can inhibit one or more of the activities of the naturally occurring form of the NOVX protein by, for example, competitively binding to a downstream or upstream member of a

cellular signaling cascade which includes the NOVX protein. Thus, specific biological effects can be elicited by treatment with a variant of limited function. In one embodiment, treatment of a subject with a variant having a subset of the biological activities of the naturally occurring form of the protein has fewer side effects in a subject relative to treatment with the naturally occurring form of the NOVX proteins.

Variants of the NOVX proteins that function as either NOVX agonists (*i.e.*, mimetics) or as NOVX antagonists can be identified by screening combinatorial libraries of mutants (*e.g.*, truncation mutants) of the NOVX proteins for NOVX protein agonist or antagonist activity. In one embodiment, a variegated library of NOVX variants is generated by combinatorial mutagenesis at the nucleic acid level and is encoded by a variegated gene library. A variegated library of NOVX variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of potential NOVX sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (*e.g.*, for phage display) containing the set of NOVX sequences therein. There are a variety of methods which can be used to produce libraries of potential NOVX variants from a degenerate oligonucleotide sequence. Chemical synthesis of a degenerate gene sequence can be performed in an automatic DNA synthesizer, and the synthetic gene then ligated into an appropriate expression vector. Use of a degenerate set of genes allows for the provision, in one mixture, of all of the sequences encoding the desired set of potential NOVX sequences. Methods for synthesizing degenerate oligonucleotides are well-known within the art. *See, e.g.*, Narang, 1983. *Tetrahedron* 39: 3; Itakura, *et al.*, 1984. *Annu. Rev. Biochem.* 53: 323; Itakura, *et al.*, 1984. *Science* 198: 1056; Ike, *et al.*, 1983. *Nucl. Acids Res.* 11: 477.

Polypeptide Libraries

In addition, libraries of fragments of the NOVX protein coding sequences can be used to generate a variegated population of NOVX fragments for screening and subsequent selection of variants of an NOVX protein. In one embodiment, a library of coding sequence fragments can be generated by treating a double stranded PCR fragment of an NOVX coding sequence with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to form double-stranded DNA that can include sense/antisense pairs from different nicked products, removing single stranded portions from reformed duplexes by treatment with S₁ nuclease, and ligating the resulting fragment library

into an expression vector. By this method, expression libraries can be derived which encodes N-terminal and internal fragments of various sizes of the NOVX proteins.

Various techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA libraries for gene products having a selected property. Such techniques are adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of NOVX proteins. The most widely used techniques, which are amenable to high throughput analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a new technique that enhances the frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify NOVX variants. See, e.g., Arkin and Yourvan, 1992. *Proc. Natl. Acad. Sci. USA* 89: 7811-7815; Delgrave, et al., 1993. *Protein Engineering* 6:327-331.

Anti-NOVX Antibodies

The invention encompasses antibodies and antibody fragments, such as F_{ab} or $(F_{ab})_2$, that bind immunospecifically to any of the NOVX polypeptides of said invention.

An isolated NOVX protein, or a portion or fragment thereof, can be used as an immunogen to generate antibodies that bind to NOVX polypeptides using standard techniques for polyclonal and monoclonal antibody preparation. The full-length NOVX proteins can be used or, alternatively, the invention provides antigenic peptide fragments of NOVX proteins for use as immunogens. The antigenic NOVX peptides comprises at least 4 amino acid residues of the amino acid sequence shown SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, or 34 and encompasses an epitope of NOVX such that an antibody raised against the peptide forms a specific immune complex with NOVX. Preferably, the antigenic peptide comprises at least 6, 8, 10, 15, 20, or 30 amino acid residues. Longer antigenic peptides are sometimes preferable over shorter antigenic peptides, depending on use and according to methods well known to someone skilled in the art.

In certain embodiments of the invention, at least one epitope encompassed by the antigenic peptide is a region of NOVX that is located on the surface of the protein (e.g., a

hydrophilic region). As a means for targeting antibody production, hydropathy plots showing regions of hydrophilicity and hydrophobicity may be generated by any method well known in the art, including, for example, the Kyte Doolittle or the Hopp Woods methods, either with or without Fourier transformation (*see, e.g.,* Hopp and Woods, 1981. *Proc. Nat. Acad. Sci. USA* 78: 3824-3828; Kyte and Doolittle, 1982. *J. Mol. Biol.* 157: 105-142, each incorporated herein by reference in their entirety).

As disclosed herein, NOVX protein sequences of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, and 34, or derivatives, fragments, analogs or homologs thereof, may be utilized as immunogens in the generation of antibodies that immunospecifically-bind these protein components. The term "antibody" as used herein refers to immunoglobulin molecules and immunologically-active portions of immunoglobulin molecules, *i.e.*, molecules that contain an antigen binding site that specifically-binds (immunoreacts with) an antigen, such as NOVX. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, F_{ab} and F_{(ab')₂} fragments, and an F_{ab} expression library. In a specific embodiment, antibodies to human NOVX proteins are disclosed. Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies to an NOVX protein sequence of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, and 34, or a derivative, fragment, analog or homolog thereof. Some of these proteins are discussed below.

For the production of polyclonal antibodies, various suitable host animals (*e.g.*, rabbit, goat, mouse or other mammal) may be immunized by injection with the native protein, or a synthetic variant thereof, or a derivative of the foregoing. An appropriate immunogenic preparation can contain, for example, recombinantly-expressed NOVX protein or a chemically-synthesized NOVX polypeptide. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (*e.g.*, aluminum hydroxide), surface active substances (*e.g.*, lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), human adjuvants such as *Bacille Calmette-Guerin* and *Corynebacterium parvum*, or similar immunostimulatory agents. If desired, the antibody molecules directed against NOVX can be isolated from the mammal (*e.g.*, from the blood) and further purified by well known techniques, such as protein A chromatography to obtain the IgG fraction.

The term "monoclonal antibody" or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one species of an antigen binding site capable of immunoreacting with a particular epitope of NOVX. A monoclonal antibody composition thus typically displays a single binding affinity for a particular NOVX protein with which it immunoreacts. For preparation of monoclonal antibodies directed towards a particular NOVX protein, or derivatives, fragments, analogs or homologs thereof, any technique that provides for the production of antibody molecules by continuous cell line culture may be utilized. Such techniques include, but are not limited to, the hybridoma technique (*see, e.g.,* Kohler & Milstein, 1975. *Nature* 256: 495-497); the trioma technique; the human B-cell hybridoma technique (*see, e.g.,* Kozbor, *et al.*, 1983. *Immunol. Today* 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (*see, e.g.,* Cole, *et al.*, 1985. In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal antibodies may be utilized in the practice of the invention and may be produced by using human hybridomas (*see, e.g.,* Cote, *et al.*, 1983. *Proc Natl Acad Sci USA* 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus *in vitro* (*see, e.g.,* Cole, *et al.*, 1985. In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Each of the above citations is incorporated herein by reference in their entirety.

According to the invention, techniques can be adapted for the production of single-chain antibodies specific to an NOVX protein (*see, e.g.,* U.S. Patent No. 4,946,778). In addition, methods can be adapted for the construction of F_{ab} expression libraries (*see, e.g.,* Huse, *et al.*, 1989. *Science* 246: 1275-1281) to allow rapid and effective identification of monoclonal F_{ab} fragments with the desired specificity for an NOVX protein or derivatives, fragments, analogs or homologs thereof. Non-human antibodies can be "humanized" by techniques well known in the art. *See, e.g.,* U.S. Patent No. 5,225,539. Antibody fragments that contain the idiotypes to an NOVX protein may be produced by techniques known in the art including, but not limited to: (i) an F_{(ab')₂} fragment produced by pepsin digestion of an antibody molecule; (ii) an F_{ab} fragment generated by reducing the disulfide bridges of an F_{(ab')₂} fragment; (iii) an F_{ab} fragment generated by the treatment of the antibody molecule with papain and a reducing agent; and (iv) F_v fragments.

Additionally, recombinant anti-NOVX antibodies, such as chimeric and humanized monoclonal antibodies, comprising both human and non-human portions, which can be made using standard recombinant DNA techniques, are within the scope of the invention. Such

chimeric and humanized monoclonal antibodies can be produced by recombinant DNA techniques known in the art, for example using methods described in International Application No. PCT/US86/02269; European Patent Application No. 184,187; European Patent Application No. 171,496; European Patent Application No. 173,494; PCT International Publication No. WO 86/01533; U.S. Patent No. 4,816,567; U.S. Pat. No. 5,225,539; European Patent Application No. 125,023; Better, *et al.*, 1988. *Science* 240: 1041-1043; Liu, *et al.*, 1987. *Proc. Natl. Acad. Sci. USA* 84: 3439-3443; Liu, *et al.*, 1987. *J. Immunol.* 139: 3521-3526; Sun, *et al.*, 1987. *Proc. Natl. Acad. Sci. USA* 84: 214-218; Nishimura, *et al.*, 1987. *Cancer Res.* 47: 999-1005; Wood, *et al.*, 1985. *Nature* 314 :446-449; Shaw, *et al.*, 1988. *J. Natl. Cancer Inst.* 80: 1553-1559); Morrison(1985) *Science* 229:1202-1207; Oi, *et al.* (1986) *BioTechniques* 4:214; Jones, *et al.*, 1986. *Nature* 321: 552-525; Verhoeyan, *et al.*, 1988. *Science* 239: 1534; and Beidler, *et al.*, 1988. *J. Immunol.* 141: 4053-4060. Each of the above citations are incorporated herein by reference in their entirety.

In one embodiment, methods for the screening of antibodies that possess the desired specificity include, but are not limited to, enzyme-linked immunosorbent assay (ELISA) and other immunologically-mediated techniques known within the art. In a specific embodiment, selection of antibodies that are specific to a particular domain of an NOVX protein is facilitated by generation of hybridomas that bind to the fragment of an NOVX protein possessing such a domain. Thus, antibodies that are specific for a desired domain within an NOVX protein, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

Anti-NOVX antibodies may be used in methods known within the art relating to the localization and/or quantitation of an NOVX protein (*e.g.*, for use in measuring levels of the NOVX protein within appropriate physiological samples, for use in diagnostic methods, for use in imaging the protein, and the like). In a given embodiment, antibodies for NOVX proteins, or derivatives, fragments, analogs or homologs thereof, that contain the antibody derived binding domain, are utilized as pharmacologically-active compounds (hereinafter "Therapeutics").

An anti-NOVX antibody (*e.g.*, monoclonal antibody) can be used to isolate an NOVX polypeptide by standard techniques, such as affinity chromatography or immunoprecipitation. An anti-NOVX antibody can facilitate the purification of natural NOVX polypeptide from cells and of recombinantly-produced NOVX polypeptide expressed in host cells. Moreover, an anti-NOVX antibody can be used to detect NOVX protein (*e.g.*, in a cellular lysate or cell supernatant) in order to evaluate the abundance and pattern of expression of the NOVX protein.

Anti-NOVX antibodies can be used diagnostically to monitor protein levels in tissue as part of a clinical testing procedure, *e.g.*, to, for example, determine the efficacy of a given treatment regimen. Detection can be facilitated by coupling (*i.e.*, physically linking) the antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, β -galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include ^{125}I , ^{131}I , ^{35}S or ^3H .

NOVX Recombinant Expression Vectors and Host Cells

Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding an NOVX protein, or derivatives, fragments, analogs or homologs thereof. As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (*e.g.*, bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*, non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively-linked. Such vectors are referred to herein as "expression vectors". In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" can be used interchangeably as the plasmid is the most commonly used form of vector. However, the invention is intended to include such other forms of expression vectors, such as viral vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, which means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, that is operatively-linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably-linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner that allows for expression of the nucleotide sequence (*e.g.*, in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell).

The term "regulatory sequence" is intended to include promoters, enhancers and other expression control elements (*e.g.*, polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990). Regulatory sequences include those that direct constitutive expression of a nucleotide sequence in many types of host cell and those that direct expression of the nucleotide sequence only in certain host cells (*e.g.*, tissue-specific regulatory sequences). It will be appreciated by those skilled in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, etc. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described herein (*e.g.*, NOVX proteins, mutant forms of NOVX proteins, fusion proteins, etc.).

The recombinant expression vectors of the invention can be designed for expression of NOVX proteins in prokaryotic or eukaryotic cells. For example, NOVX proteins can be expressed in bacterial cells such as *Escherichia coli*, insect cells (using baculovirus expression vectors) yeast cells or mammalian cells. Suitable host cells are discussed further in Goeddel, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990). Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

Expression of proteins in prokaryotes is most often carried out in *Escherichia coli* with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion proteins. Fusion vectors add a number of amino acids to a protein encoded therein, usually to the amino terminus of the recombinant protein. Such fusion vectors typically

serve three purposes: (i) to increase expression of recombinant protein; (ii) to increase the solubility of the recombinant protein; and (iii) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the recombinant protein to enable separation of the recombinant protein from the fusion moiety subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase. Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith and Johnson, 1988. *Gene* 67: 31-40), pMAL (New England Biolabs, Beverly, Mass.) and pRIT5 (Pharmacia, Piscataway, N.J.) that fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein.

Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amrann *et al.*, (1988) *Gene* 69:301-315) and pET 11d (Studier *et al.*, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990) 60-89).

One strategy to maximize recombinant protein expression in *E. coli* is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein. *See, e.g.*, Gottesman, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990) 119-128. Another strategy is to alter the nucleic acid sequence of the nucleic acid to be inserted into an expression vector so that the individual codons for each amino acid are those preferentially utilized in *E. coli* (*see, e.g.*, Wada, *et al.*, 1992. *Nucl. Acids Res.* 20: 2111-2118). Such alteration of nucleic acid sequences of the invention can be carried out by standard DNA synthesis techniques.

In another embodiment, the NOVX expression vector is a yeast expression vector. Examples of vectors for expression in yeast *Saccharomyces cerevisiae* include pYepSec1 (Baldari, *et al.*, 1987. *EMBO J.* 6: 229-234), pMFa (Kurjan and Herskowitz, 1982. *Cell* 30: 933-943), pJRY88 (Schultz *et al.*, 1987. *Gene* 54: 113-123), pYES2 (Invitrogen Corporation, San Diego, Calif.), and picZ (Invitrogen Corp, San Diego, Calif.).

Alternatively, NOVX can be expressed in insect cells using baculovirus expression vectors. Baculovirus vectors available for expression of proteins in cultured insect cells (*e.g.*, SF9 cells) include the pAc series (Smith, *et al.*, 1983. *Mol. Cell. Biol.* 3: 2156-2165) and the pVL series (Lucklow and Summers, 1989. *Virology* 170: 31-39).

In yet another embodiment, a nucleic acid of the invention is expressed in mammalian cells using a mammalian expression vector. Examples of mammalian expression vectors include pCDM8 (Seed, 1987. *Nature* 329: 840) and pMT2PC (Kaufman, *et al.*, 1987. *EMBO J.* 6: 187-195). When used in mammalian cells, the expression vector's control functions are often provided by viral regulatory elements. For example, commonly used promoters are derived from polyoma, adenovirus 2, cytomegalovirus, and simian virus 40. For other suitable expression systems for both prokaryotic and eukaryotic cells see, *e.g.*, Chapters 16 and 17 of Sambrook, *et al.*, MOLECULAR CLONING: A LABORATORY MANUAL. 2nd ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989.

In another embodiment, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type (*e.g.*, tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific; Pinkert, *et al.*, 1987. *Genes Dev.* 1: 268-277), lymphoid-specific promoters (Calame and Eaton, 1988. *Adv. Immunol.* 43: 235-275), in particular promoters of T cell receptors (Winoto and Baltimore, 1989. *EMBO J.* 8: 729-733) and immunoglobulins (Banerji, *et al.*, 1983. *Cell* 33: 729-740; Queen and Baltimore, 1983. *Cell* 33: 741-748), neuron-specific promoters (*e.g.*, the neurofilament promoter; Byrne and Ruddle, 1989. *Proc. Natl. Acad. Sci. USA* 86: 5473-5477), pancreas-specific promoters (Edlund, *et al.*, 1985. *Science* 230: 912-916), and mammary gland-specific promoters (*e.g.*, milk whey promoter; U.S. Pat. No. 4,873,316 and European Application Publication No. 264,166). Developmentally-regulated promoters are also encompassed, *e.g.*, the murine hox promoters (Kessel and Gruss, 1990. *Science* 249: 374-379) and the α -fetoprotein promoter (Campes and Tilghman, 1989. *Genes Dev.* 3: 537-546).

The invention further provides a recombinant expression vector comprising a DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operatively-linked to a regulatory sequence in a manner that allows for expression (by transcription of the DNA molecule) of an RNA molecule that is antisense to NOVX mRNA. Regulatory sequences operatively linked to a nucleic acid cloned in the antisense orientation can be chosen that direct the continuous expression of the antisense RNA molecule in a variety of cell types, for instance viral promoters and/or enhancers, or regulatory sequences can be chosen that direct constitutive, tissue specific or cell type specific expression

of antisense RNA. The antisense expression vector can be in the form of a recombinant plasmid, phagemid or attenuated virus in which antisense nucleic acids are produced under the control of a high efficiency regulatory region, the activity of which can be determined by the cell type into which the vector is introduced. For a discussion of the regulation of gene expression using antisense genes *see, e.g.,* Weintraub, *et al.*, "Antisense RNA as a molecular tool for genetic analysis," *Reviews-Trends in Genetics*, Vol. 1(1) 1986.

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but also to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic or eukaryotic cell. For example, NOVX protein can be expressed in bacterial cells such as *E. coli*, insect cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to those skilled in the art.

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (*e.g.,* DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, *et al.* (MOLECULAR CLONING: A LABORATORY MANUAL. 2nd ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989), and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (*e.g.,* resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Various selectable markers include those that confer resistance to drugs, such as G418, hygromycin and methotrexate. Nucleic acid encoding a

selectable marker can be introduced into a host cell on the same vector as that encoding NOVX or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid can be identified by drug selection (*e.g.*, cells that have incorporated the selectable marker gene will survive, while the other cells die).

5 A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (*i.e.*, express) NOVX protein. Accordingly, the invention further provides methods for producing NOVX protein using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding NOVX protein has been introduced) in a suitable
10 medium such that NOVX protein is produced. In another embodiment, the method further comprises isolating NOVX protein from the medium or the host cell.

Transgenic NOVX Animals

 The host cells of the invention can also be used to produce non-human transgenic animals. For example, in one embodiment, a host cell of the invention is a fertilized oocyte or
15 an embryonic stem cell into which NOVX protein-coding sequences have been introduced. Such host cells can then be used to create non-human transgenic animals in which exogenous NOVX sequences have been introduced into their genome or homologous recombinant animals in which endogenous NOVX sequences have been altered. Such animals are useful for studying the function and/or activity of NOVX protein and for identifying and/or evaluating
20 modulators of NOVX protein activity. As used herein, a "transgenic animal" is a non-human animal, preferably a mammal, more preferably a rodent such as a rat or mouse, in which one or more of the cells of the animal includes a transgene. Other examples of transgenic animals include non-human primates, sheep, dogs, cows, goats, chickens, amphibians, etc. A transgene is exogenous DNA that is integrated into the genome of a cell from which a transgenic animal
25 develops and that remains in the genome of the mature animal, thereby directing the expression of an encoded gene product in one or more cell types or tissues of the transgenic animal. As used herein, a "homologous recombinant animal" is a non-human animal, preferably a mammal, more preferably a mouse, in which an endogenous NOVX gene has been altered by homologous recombination between the endogenous gene and an exogenous DNA molecule
30 introduced into a cell of the animal, *e.g.*, an embryonic cell of the animal, prior to development of the animal.

A transgenic animal of the invention can be created by introducing NOVX-encoding nucleic acid into the male pronuclei of a fertilized oocyte (*e.g.*, by microinjection, retroviral infection) and allowing the oocyte to develop in a pseudopregnant female foster animal. The human NOVX cDNA sequences SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, or 33 can be introduced as a transgene into the genome of a non-human animal.

Alternatively, a non-human homologue of the human NOVX gene, such as a mouse NOVX gene, can be isolated based on hybridization to the human NOVX cDNA (described further *supra*) and used as a transgene. Intronic sequences and polyadenylation signals can also be included in the transgene to increase the efficiency of expression of the transgene. A tissue-specific regulatory sequence(s) can be operably-linked to the NOVX transgene to direct expression of NOVX protein to particular cells. Methods for generating transgenic animals via embryo manipulation and microinjection, particularly animals such as mice, have become conventional in the art and are described, for example, in U.S. Patent Nos. 4,736,866; 4,870,009; and 4,873,191; and Hogan, 1986. In: MANIPULATING THE MOUSE EMBRYO, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. Similar methods are used for production of other transgenic animals. A transgenic founder animal can be identified based upon the presence of the NOVX transgene in its genome and/or expression of NOVX mRNA in tissues or cells of the animals. A transgenic founder animal can then be used to breed additional animals carrying the transgene. Moreover, transgenic animals carrying a transgene-encoding NOVX protein can further be bred to other transgenic animals carrying other transgenes.

To create a homologous recombinant animal, a vector is prepared which contains at least a portion of an NOVX gene into which a deletion, addition or substitution has been introduced to thereby alter, *e.g.*, functionally disrupt, the NOVX gene. The NOVX gene can be a human gene (*e.g.*, the cDNA of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, or 33), but more preferably, is a non-human homologue of a human NOVX gene. For example, a mouse homologue of human NOVX gene of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, or 33 can be used to construct a homologous recombination vector suitable for altering an endogenous NOVX gene in the mouse genome. In one embodiment, the vector is designed such that, upon homologous recombination, the endogenous NOVX gene is functionally disrupted (*i.e.*, no longer encodes a functional protein; also referred to as a "knock out" vector).

Alternatively, the vector can be designed such that, upon homologous recombination, the endogenous NOVX gene is mutated or otherwise altered but still encodes functional protein (e.g., the upstream regulatory region can be altered to thereby alter the expression of the endogenous NOVX protein). In the homologous recombination vector, the altered portion of the NOVX gene is flanked at its 5'- and 3'-termini by additional nucleic acid of the NOVX gene to allow for homologous recombination to occur between the exogenous NOVX gene carried by the vector and an endogenous NOVX gene in an embryonic stem cell. The additional flanking NOVX nucleic acid is of sufficient length for successful homologous recombination with the endogenous gene. Typically, several kilobases of flanking DNA (both at the 5'- and 3'-termini) are included in the vector. *See, e.g., Thomas, et al., 1987. Cell 51: 503 for a description of homologous recombination vectors. The vector is then introduced into an embryonic stem cell line (e.g., by electroporation) and cells in which the introduced NOVX gene has homologously-recombined with the endogenous NOVX gene are selected. See, e.g., Li, et al., 1992. Cell 69: 915.*

The selected cells are then injected into a blastocyst of an animal (e.g., a mouse) to form aggregation chimeras. *See, e.g., Bradley, 1987. In: TERATOCARCINOMAS AND EMBRYONIC STEM CELLS: A PRACTICAL APPROACH, Robertson, ed. IRL, Oxford, pp. 113-152. A chimeric embryo can then be implanted into a suitable pseudopregnant female foster animal and the embryo brought to term. Progeny harboring the homologously-recombined DNA in their germ cells can be used to breed animals in which all cells of the animal contain the homologously-recombined DNA by germline transmission of the transgene. Methods for constructing homologous recombination vectors and homologous recombinant animals are described further in Bradley, 1991. Curr. Opin. Biotechnol. 2: 823-829; PCT International Publication Nos.: WO 90/11354; WO 91/01140; WO 92/0968; and WO 93/04169.*

In another embodiment, transgenic non-humans animals can be produced that contain selected systems that allow for regulated expression of the transgene. One example of such a system is the cre/loxP recombinase system of bacteriophage P1. For a description of the cre/loxP recombinase system, *See, e.g., Lakso, et al., 1992. Proc. Natl. Acad. Sci. USA 89: 6232-6236. Another example of a recombinase system is the FLP recombinase system of Saccharomyces cerevisiae. See, O'Gorman, et al., 1991. Science 251:1351-1355. If a cre/loxP recombinase system is used to regulate expression of the transgene, animals containing transgenes encoding both the Cre recombinase and a selected protein are required. Such*

animals can be provided through the construction of "double" transgenic animals, *e.g.*, by mating two transgenic animals, one containing a transgene encoding a selected protein and the other containing a transgene encoding a recombinase.

Clones of the non-human transgenic animals described herein can also be produced according to the methods described in Wilmut, *et al.*, 1997. *Nature* 385: 810-813. In brief, a cell (*e.g.*, a somatic cell) from the transgenic animal can be isolated and induced to exit the growth cycle and enter G₀ phase. The quiescent cell can then be fused, *e.g.*, through the use of electrical pulses, to an enucleated oocyte from an animal of the same species from which the quiescent cell is isolated. The reconstructed oocyte is then cultured such that it develops to morula or blastocyte and then transferred to pseudopregnant female foster animal. The offspring borne of this female foster animal will be a clone of the animal from which the cell (*e.g.*, the somatic cell) is isolated.

Pharmaceutical Compositions

The NOVX nucleic acid molecules, NOVX proteins, and anti-NOVX antibodies (also referred to herein as "active compounds") of the invention, and derivatives, fragments, analogs and homologs thereof, can be incorporated into pharmaceutical compositions suitable for administration. Such compositions typically comprise the nucleic acid molecule, protein, or antibody and a pharmaceutically acceptable carrier. As used herein, "pharmaceutically acceptable carrier" is intended to include any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like, compatible with pharmaceutical administration. Suitable carriers are described in the most recent edition of Remington's Pharmaceutical Sciences, a standard reference text in the field, which is incorporated herein by reference. Preferred examples of such carriers or diluents include, but are not limited to, water, saline, finger's solutions, dextrose solution, and 5% human serum albumin. Liposomes and non-aqueous vehicles such as fixed oils may also be used. The use of such media and agents for pharmaceutically active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the active compound, use thereof in the compositions is contemplated. Supplementary active compounds can also be incorporated into the compositions.

A pharmaceutical composition of the invention is formulated to be compatible with its intended route of administration. Examples of routes of administration include parenteral, *e.g.*,

intravenous, intradermal, subcutaneous, oral (*e.g.*, inhalation), transdermal (*i.e.*, topical), transmucosal, and rectal administration. Solutions or suspensions used for parenteral, intradermal, or subcutaneous application can include the following components: a sterile diluent such as water for injection, saline solution, fixed oils, polyethylene glycols, glycerine, propylene glycol or other synthetic solvents; antibacterial agents such as benzyl alcohol or methyl parabens; antioxidants such as ascorbic acid or sodium bisulfite; chelating agents such as ethylenediaminetetraacetic acid (EDTA); buffers such as acetates, citrates or phosphates, and agents for the adjustment of tonicity such as sodium chloride or dextrose. The pH can be adjusted with acids or bases, such as hydrochloric acid or sodium hydroxide. The parenteral preparation can be enclosed in ampoules, disposable syringes or multiple dose vials made of glass or plastic.

Pharmaceutical compositions suitable for injectable use include sterile aqueous solutions (where water soluble) or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersion. For intravenous administration, suitable carriers include physiological saline, bacteriostatic water, Cremophor EL™ (BASF, Parsippany, N.J.) or phosphate buffered saline (PBS). In all cases, the composition must be sterile and should be fluid to the extent that easy syringeability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), and suitable mixtures thereof. The proper fluidity can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. Prevention of the action of microorganisms can be achieved by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, ascorbic acid, thimerosal, and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars, polyalcohols such as manitol, sorbitol, sodium chloride in the composition. Prolonged absorption of the injectable compositions can be brought about by including in the composition an agent which delays absorption, for example, aluminum monostearate and gelatin.

Sterile injectable solutions can be prepared by incorporating the active compound (*e.g.*, an NOVX protein or anti-NOVX antibody) in the required amount in an appropriate solvent with one or a combination of ingredients enumerated above, as required, followed by filtered

sterilization. Generally, dispersions are prepared by incorporating the active compound into a sterile vehicle that contains a basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, methods of preparation are vacuum drying and freeze-drying that yields a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof.

Oral compositions generally include an inert diluent or an edible carrier. They can be enclosed in gelatin capsules or compressed into tablets. For the purpose of oral therapeutic administration, the active compound can be incorporated with excipients and used in the form of tablets, troches, or capsules. Oral compositions can also be prepared using a fluid carrier for use as a mouthwash, wherein the compound in the fluid carrier is applied orally and swished and expectorated or swallowed. Pharmaceutically compatible binding agents, and/or adjuvant materials can be included as part of the composition. The tablets, pills, capsules, troches and the like can contain any of the following ingredients, or compounds of a similar nature: a binder such as microcrystalline cellulose, gum tragacanth or gelatin; an excipient such as starch or lactose, a disintegrating agent such as alginic acid, Primogel, or corn starch; a lubricant such as magnesium stearate or Sterotes; a glidant such as colloidal silicon dioxide; a sweetening agent such as sucrose or saccharin; or a flavoring agent such as peppermint, methyl salicylate, or orange flavoring.

For administration by inhalation, the compounds are delivered in the form of an aerosol spray from pressured container or dispenser which contains a suitable propellant, *e.g.*, a gas such as carbon dioxide, or a nebulizer.

Systemic administration can also be by transmucosal or transdermal means. For transmucosal or transdermal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art, and include, for example, for transmucosal administration, detergents, bile salts, and fusidic acid derivatives. Transmucosal administration can be accomplished through the use of nasal sprays or suppositories. For transdermal administration, the active compounds are formulated into ointments, salves, gels, or creams as generally known in the art.

The compounds can also be prepared in the form of suppositories (*e.g.*, with conventional suppository bases such as cocoa butter and other glycerides) or retention enemas for rectal delivery.

In one embodiment, the active compounds are prepared with carriers that will protect the compound against rapid elimination from the body, such as a controlled release formulation, including implants and microencapsulated delivery systems. Biodegradable, biocompatible polymers can be used, such as ethylene vinyl acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, and polylactic acid. Methods for preparation of such formulations will be apparent to those skilled in the art. The materials can also be obtained commercially from Alza Corporation and Nova Pharmaceuticals, Inc. Liposomal suspensions (including liposomes targeted to infected cells with monoclonal antibodies to viral antigens) can also be used as pharmaceutically acceptable carriers. These can be prepared according to methods known to those skilled in the art, for example, as described in U.S. Patent No. 4,522,811.

It is especially advantageous to formulate oral or parenteral compositions in dosage unit form for ease of administration and uniformity of dosage. Dosage unit form as used herein refers to physically discrete units suited as unitary dosages for the subject to be treated; each unit containing a predetermined quantity of active compound calculated to produce the desired therapeutic effect in association with the required pharmaceutical carrier. The specification for the dosage unit forms of the invention are dictated by and directly dependent on the unique characteristics of the active compound and the particular therapeutic effect to be achieved, and the limitations inherent in the art of compounding such an active compound for the treatment of individuals.

The nucleic acid molecules of the invention can be inserted into vectors and used as gene therapy vectors. Gene therapy vectors can be delivered to a subject by, for example, intravenous injection, local administration (*see, e.g.*, U.S. Patent No. 5,328,470) or by stereotactic injection (*see, e.g.*, Chen, *et al.*, 1994. *Proc. Natl. Acad. Sci. USA* 91: 3054-3057). The pharmaceutical preparation of the gene therapy vector can include the gene therapy vector in an acceptable diluent, or can comprise a slow release matrix in which the gene delivery vehicle is imbedded. Alternatively, where the complete gene delivery vector can be produced intact from recombinant cells, *e.g.*, retroviral vectors, the pharmaceutical preparation can include one or more cells that produce the gene delivery system.

The pharmaceutical compositions can be included in a container, pack, or dispenser together with instructions for administration.

Screening and Detection Methods

The isolated nucleic acid molecules of the invention can be used to express NOVX protein (*e.g.*, via a recombinant expression vector in a host cell in gene therapy applications), to detect NOVX mRNA (*e.g.*, in a biological sample) or a genetic lesion in an NOVX gene, and to modulate NOVX activity, as described further, below. In addition, the NOVX proteins can be used to screen drugs or compounds that modulate the NOVX protein activity or expression as well as to treat disorders characterized by insufficient or excessive production of NOVX protein or production of NOVX protein forms that have decreased or aberrant activity compared to NOVX wild-type protein (*e.g.*; diabetes (regulates insulin release); obesity (binds and transport lipids); metabolic disturbances associated with obesity, the metabolic syndrome X as well as anorexia and wasting disorders associated with chronic diseases and various cancers, and infectious disease (possesses anti-microbial activity) and the various dyslipidemias. In addition, the anti-NOVX antibodies of the invention can be used to detect and isolate NOVX proteins and modulate NOVX activity. In yet a further aspect, the invention can be used in methods to influence appetite, absorption of nutrients and the disposition of metabolic substrates in both a positive and negative fashion.

The invention further pertains to novel agents identified by the screening assays described herein and uses thereof for treatments as described, *supra*.

Screening Assays

The invention provides a method (also referred to herein as a "screening assay") for identifying modulators, *i.e.*, candidate or test compounds or agents (*e.g.*, peptides, peptidomimetics, small molecules or other drugs) that bind to NOVX proteins or have a stimulatory or inhibitory effect on, *e.g.*, NOVX protein expression or NOVX protein activity.

The invention also includes compounds identified in the screening assays described herein.

In one embodiment, the invention provides assays for screening candidate or test compounds which bind to or modulate the activity of the membrane-bound form of an NOVX protein or polypeptide or biologically-active portion thereof. The test compounds of the invention can be obtained using any of the numerous approaches in combinatorial library methods known in the art, including: biological libraries; spatially addressable parallel solid phase or solution phase libraries; synthetic library methods requiring deconvolution; the "one-bead one-compound" library method; and synthetic library methods using affinity

chromatography selection. The biological library approach is limited to peptide libraries, while the other four approaches are applicable to peptide, non-peptide oligomer or small molecule libraries of compounds. *See, e.g., Lam, 1997. Anticancer Drug Design 12: 145.*

A "small molecule" as used herein, is meant to refer to a composition that has a molecular weight of less than about 5 kD and most preferably less than about 4 kD. Small molecules can be, *e.g.,* nucleic acids, peptides, polypeptides, peptidomimetics, carbohydrates, lipids or other organic or inorganic molecules. Libraries of chemical and/or biological mixtures, such as fungal, bacterial, or algal extracts, are known in the art and can be screened with any of the assays of the invention.

Examples of methods for the synthesis of molecular libraries can be found in the art, for example in: DeWitt, *et al.*, 1993. *Proc. Natl. Acad. Sci. U.S.A.* 90: 6909; Erb, *et al.*, 1994. *Proc. Natl. Acad. Sci. U.S.A.* 91: 11422; Zuckermann, *et al.*, 1994. *J. Med. Chem.* 37: 2678; Cho, *et al.*, 1993. *Science* 261: 1303; Carrell, *et al.*, 1994. *Angew. Chem. Int. Ed. Engl.* 33: 2059; Carrell, *et al.*, 1994. *Angew. Chem. Int. Ed. Engl.* 33: 2061; and Gallop, *et al.*, 1994. *J. Med. Chem.* 37: 1233.

Libraries of compounds may be presented in solution (*e.g.,* Houghten, 1992. *Biotechniques* 13: 412-421), or on beads (Lam, 1991. *Nature* 354: 82-84), on chips (Fodor, 1993. *Nature* 364: 555-556), bacteria (Ladner, U.S. Patent No. 5,223,409), spores (Ladner, U.S. Patent 5,233,409), plasmids (Cull, *et al.*, 1992. *Proc. Natl. Acad. Sci. USA* 89: 1865-1869) or on phage (Scott and Smith, 1990. *Science* 249: 386-390; Devlin, 1990. *Science* 249: 404-406; Cwirla, *et al.*, 1990. *Proc. Natl. Acad. Sci. U.S.A.* 87: 6378-6382; Felici, 1991. *J. Mol. Biol.* 222: 301-310; Ladner, U.S. Patent No. 5,233,409.).

In one embodiment, an assay is a cell-based assay in which a cell which expresses a membrane-bound form of NOVX protein, or a biologically-active portion thereof, on the cell surface is contacted with a test compound and the ability of the test compound to bind to an NOVX protein determined. The cell, for example, can be of mammalian origin or a yeast cell. Determining the ability of the test compound to bind to the NOVX protein can be accomplished, for example, by coupling the test compound with a radioisotope or enzymatic label such that binding of the test compound to the NOVX protein or biologically-active portion thereof can be determined by detecting the labeled compound in a complex. For example, test compounds can be labeled with ^{125}I , ^{35}S , ^{14}C , or ^3H , either directly or indirectly, and the radioisotope detected by direct counting of radioemission or by scintillation counting.

Alternatively, test compounds can be enzymatically-labeled with, for example, horseradish peroxidase, alkaline phosphatase, or luciferase, and the enzymatic label detected by determination of conversion of an appropriate substrate to product. In one embodiment, the assay comprises contacting a cell which expresses a membrane-bound form of NOVX protein, or a biologically-active portion thereof, on the cell surface with a known compound which binds NOVX to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with an NOVX protein, wherein determining the ability of the test compound to interact with an NOVX protein comprises determining the ability of the test compound to preferentially bind to NOVX protein or a biologically-active portion thereof as compared to the known compound.

In another embodiment, an assay is a cell-based assay comprising contacting a cell expressing a membrane-bound form of NOVX protein, or a biologically-active portion thereof, on the cell surface with a test compound and determining the ability of the test compound to modulate (*e.g.*, stimulate or inhibit) the activity of the NOVX protein or biologically-active portion thereof. Determining the ability of the test compound to modulate the activity of NOVX or a biologically-active portion thereof can be accomplished, for example, by determining the ability of the NOVX protein to bind to or interact with an NOVX target molecule. As used herein, a "target molecule" is a molecule with which an NOVX protein binds or interacts in nature, for example, a molecule on the surface of a cell which expresses an NOVX interacting protein, a molecule on the surface of a second cell, a molecule in the extracellular milieu, a molecule associated with the internal surface of a cell membrane or a cytoplasmic molecule. An NOVX target molecule can be a non-NOVX molecule or an NOVX protein or polypeptide of the invention. In one embodiment, an NOVX target molecule is a component of a signal transduction pathway that facilitates transduction of an extracellular signal (*e.g.* a signal generated by binding of a compound to a membrane-bound NOVX molecule) through the cell membrane and into the cell. The target, for example, can be a second intercellular protein that has catalytic activity or a protein that facilitates the association of downstream signaling molecules with NOVX.

Determining the ability of the NOVX protein to bind to or interact with an NOVX target molecule can be accomplished by one of the methods described above for determining direct binding. In one embodiment, determining the ability of the NOVX protein to bind to or interact with an NOVX target molecule can be accomplished by determining the activity of the target

molecule. For example, the activity of the target molecule can be determined by detecting induction of a cellular second messenger of the target (*i.e.* intracellular Ca^{2+} , diacylglycerol, IP_3 , etc.), detecting catalytic/enzymatic activity of the target an appropriate substrate, detecting the induction of a reporter gene (comprising an NOVX-responsive regulatory element
5 operatively linked to a nucleic acid encoding a detectable marker, *e.g.*, luciferase), or detecting a cellular response, for example, cell survival, cellular differentiation, or cell proliferation.

In yet another embodiment, an assay of the invention is a cell-free assay comprising contacting an NOVX protein or biologically-active portion thereof with a test compound and determining the ability of the test compound to bind to the NOVX protein or biologically-active
10 portion thereof. Binding of the test compound to the NOVX protein can be determined either directly or indirectly as described above. In one such embodiment, the assay comprises contacting the NOVX protein or biologically-active portion thereof with a known compound which binds NOVX to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with an NOVX protein,
15 wherein determining the ability of the test compound to interact with an NOVX protein comprises determining the ability of the test compound to preferentially bind to NOVX or biologically-active portion thereof as compared to the known compound.

In still another embodiment, an assay is a cell-free assay comprising contacting NOVX protein or biologically-active portion thereof with a test compound and determining the ability
20 of the test compound to modulate (*e.g.* stimulate or inhibit) the activity of the NOVX protein or biologically-active portion thereof. Determining the ability of the test compound to modulate the activity of NOVX can be accomplished, for example, by determining the ability of the NOVX protein to bind to an NOVX target molecule by one of the methods described above for determining direct binding. In an alternative embodiment, determining the ability of the test
25 compound to modulate the activity of NOVX protein can be accomplished by determining the ability of the NOVX protein further modulate an NOVX target molecule. For example, the catalytic/enzymatic activity of the target molecule on an appropriate substrate can be determined as described, *supra*.

In yet another embodiment, the cell-free assay comprises contacting the NOVX protein
30 or biologically-active portion thereof with a known compound which binds NOVX protein to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with an NOVX protein, wherein determining the ability

of the test compound to interact with an NOVX protein comprises determining the ability of the NOVX protein to preferentially bind to or modulate the activity of an NOVX target molecule.

The cell-free assays of the invention are amenable to use of both the soluble form or the membrane-bound form of NOVX protein. In the case of cell-free assays comprising the membrane-bound form of NOVX protein, it may be desirable to utilize a solubilizing agent such that the membrane-bound form of NOVX protein is maintained in solution. Examples of such solubilizing agents include non-ionic detergents such as n-octylglucoside, n-dodecylglucoside, n-dodecylmaltoside, octanoyl-N-methylglucamide, decanoyl-N-methylglucamide, Triton[®] X-100, Triton[®] X-114, Thesit[®], Isotridecypoly(ethylene glycol ether)_n, N-dodecyl--N,N-dimethyl-3-ammonio-1-propane sulfonate, 3-(3-cholamidopropyl) dimethylamminiol-1-propane sulfonate (CHAPS), or 3-(3-cholamidopropyl)dimethylamminiol-2-hydroxy-1-propane sulfonate (CHAPSO).

In more than one embodiment of the above assay methods of the invention, it may be desirable to immobilize either NOVX protein or its target molecule to facilitate separation of complexed from uncomplexed forms of one or both of the proteins, as well as to accommodate automation of the assay. Binding of a test compound to NOVX protein, or interaction of NOVX protein with a target molecule in the presence and absence of a candidate compound, can be accomplished in any vessel suitable for containing the reactants. Examples of such vessels include microtiter plates, test tubes, and micro-centrifuge tubes. In one embodiment, a fusion protein can be provided that adds a domain that allows one or both of the proteins to be bound to a matrix. For example, GST-NOVX fusion proteins or GST-target fusion proteins can be adsorbed onto glutathione sepharose beads (Sigma Chemical, St. Louis, MO) or glutathione derivatized microtiter plates, that are then combined with the test compound or the test compound and either the non-adsorbed target protein or NOVX protein, and the mixture is incubated under conditions conducive to complex formation (*e.g.*, at physiological conditions for salt and pH). Following incubation, the beads or microtiter plate wells are washed to remove any unbound components, the matrix immobilized in the case of beads, complex determined either directly or indirectly, for example, as described, *supra*. Alternatively, the complexes can be dissociated from the matrix, and the level of NOVX protein binding or activity determined using standard techniques.

Other techniques for immobilizing proteins on matrices can also be used in the screening assays of the invention. For example, either the NOVX protein or its target molecule

can be immobilized utilizing conjugation of biotin and streptavidin. Biotinylated NOVX protein or target molecules can be prepared from biotin-NHS (N-hydroxy-succinimide) using techniques well-known within the art (e.g., biotinylation kit, Pierce Chemicals, Rockford, Ill.), and immobilized in the wells of streptavidin-coated 96 well plates (Pierce Chemical).

5 Alternatively, antibodies reactive with NOVX protein or target molecules, but which do not interfere with binding of the NOVX protein to its target molecule, can be derivatized to the wells of the plate, and unbound target or NOVX protein trapped in the wells by antibody conjugation. Methods for detecting such complexes, in addition to those described above for the GST-immobilized complexes, include immunodetection of complexes using antibodies
10 reactive with the NOVX protein or target molecule, as well as enzyme-linked assays that rely on detecting an enzymatic activity associated with the NOVX protein or target molecule.

In another embodiment, modulators of NOVX protein expression are identified in a method wherein a cell is contacted with a candidate compound and the expression of NOVX mRNA or protein in the cell is determined. The level of expression of NOVX mRNA or
15 protein in the presence of the candidate compound is compared to the level of expression of NOVX mRNA or protein in the absence of the candidate compound. The candidate compound can then be identified as a modulator of NOVX mRNA or protein expression based upon this comparison. For example, when expression of NOVX mRNA or protein is greater (*i.e.*, statistically significantly greater) in the presence of the candidate compound than in its absence,
20 the candidate compound is identified as a stimulator of NOVX mRNA or protein expression. Alternatively, when expression of NOVX mRNA or protein is less (statistically significantly less) in the presence of the candidate compound than in its absence, the candidate compound is identified as an inhibitor of NOVX mRNA or protein expression. The level of NOVX mRNA or protein expression in the cells can be determined by methods described herein for detecting
25 NOVX mRNA or protein.

In yet another aspect of the invention, the NOVX proteins can be used as "bait proteins" in a two-hybrid assay or three hybrid assay (*see, e.g.*, U.S. Patent No. 5,283,317; Zervos, *et al.*, 1993. *Cell* 72: 223-232; Madura, *et al.*, 1993. *J. Biol. Chem.* 268: 12046-12054; Bartel, *et al.*, 1993. *Biotechniques* 14: 920-924; Iwabuchi, *et al.*, 1993. *Oncogene* 8: 1693-1696; and Brent
30 WO 94/10300), to identify other proteins that bind to or interact with NOVX ("NOVX-binding proteins" or "NOVX-bp") and modulate NOVX activity. Such NOVX-binding proteins are also

likely to be involved in the propagation of signals by the NOVX proteins as, for example, upstream or downstream elements of the NOVX pathway.

The two-hybrid system is based on the modular nature of most transcription factors, which consist of separable DNA-binding and activation domains. Briefly, the assay utilizes two different DNA constructs. In one construct, the gene that codes for NOVX is fused to a gene encoding the DNA binding domain of a known transcription factor (*e.g.*, GAL-4). In the other construct, a DNA sequence, from a library of DNA sequences, that encodes an unidentified protein ("prey" or "sample") is fused to a gene that codes for the activation domain of the known transcription factor. If the "bait" and the "prey" proteins are able to interact, *in vivo*, forming an NOVX-dependent complex, the DNA-binding and activation domains of the transcription factor are brought into close proximity. This proximity allows transcription of a reporter gene (*e.g.*, LacZ) that is operably linked to a transcriptional regulatory site responsive to the transcription factor. Expression of the reporter gene can be detected and cell colonies containing the functional transcription factor can be isolated and used to obtain the cloned gene that encodes the protein which interacts with NOVX.

The invention further pertains to novel agents identified by the aforementioned screening assays and uses thereof for treatments as described herein.

Detection Assays

Portions or fragments of the cDNA sequences identified herein (and the corresponding complete gene sequences) can be used in numerous ways as polynucleotide reagents. By way of example, and not of limitation, these sequences can be used to: (i) map their respective genes on a chromosome; and, thus, locate gene regions associated with genetic disease; (ii) identify an individual from a minute biological sample (tissue typing); and (iii) aid in forensic identification of a biological sample. Some of these applications are described in the subsections, below.

Chromosome Mapping

Once the sequence (or a portion of the sequence) of a gene has been isolated, this sequence can be used to map the location of the gene on a chromosome. This process is called chromosome mapping. Accordingly, portions or fragments of the NOVX sequences, SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, or 33, or fragments or derivatives

thereof, can be used to map the location of the NOVX genes, respectively, on a chromosome. The mapping of the NOVX sequences to chromosomes is an important first step in correlating these sequences with genes associated with disease.

Briefly, NOVX genes can be mapped to chromosomes by preparing PCR primers (preferably 15-25 bp in length) from the NOVX sequences. Computer analysis of the NOVX sequences can be used to rapidly select primers that do not span more than one exon in the genomic DNA, thus complicating the amplification process. These primers can then be used for PCR screening of somatic cell hybrids containing individual human chromosomes. Only those hybrids containing the human gene corresponding to the NOVX sequences will yield an amplified fragment.

Somatic cell hybrids are prepared by fusing somatic cells from different mammals (*e.g.*, human and mouse cells). As hybrids of human and mouse cells grow and divide, they gradually lose human chromosomes in random order, but retain the mouse chromosomes. By using media in which mouse cells cannot grow, because they lack a particular enzyme, but in which human cells can, the one human chromosome that contains the gene encoding the needed enzyme will be retained. By using various media, panels of hybrid cell lines can be established. Each cell line in a panel contains either a single human chromosome or a small number of human chromosomes, and a full set of mouse chromosomes, allowing easy mapping of individual genes to specific human chromosomes. *See, e.g., D'Eustachio, et al., 1983. Science* 220: 919-924. Somatic cell hybrids containing only fragments of human chromosomes can also be produced by using human chromosomes with translocations and deletions.

PCR mapping of somatic cell hybrids is a rapid procedure for assigning a particular sequence to a particular chromosome. Three or more sequences can be assigned per day using a single thermal cycler. Using the NOVX sequences to design oligonucleotide primers, sub-localization can be achieved with panels of fragments from specific chromosomes.

Fluorescence *in situ* hybridization (FISH) of a DNA sequence to a metaphase chromosomal spread can further be used to provide a precise chromosomal location in one step. Chromosome spreads can be made using cells whose division has been blocked in metaphase by a chemical like colcemid that disrupts the mitotic spindle. The chromosomes can be treated briefly with trypsin, and then stained with Giemsa. A pattern of light and dark bands develops on each chromosome, so that the chromosomes can be identified individually. The FISH technique can be used with a DNA sequence as short as 500 or 600 bases. However, clones

larger than 1,000 bases have a higher likelihood of binding to a unique chromosomal location with sufficient signal intensity for simple detection. Preferably 1,000 bases, and more preferably 2,000 bases, will suffice to get good results at a reasonable amount of time. For a review of this technique, *see*, Verma, *et al.*, HUMAN CHROMOSOMES: A MANUAL OF BASIC
5 TECHNIQUES (Pergamon Press, New York 1988).

Reagents for chromosome mapping can be used individually to mark a single chromosome or a single site on that chromosome, or panels of reagents can be used for marking multiple sites and/or multiple chromosomes. Reagents corresponding to noncoding regions of the genes actually are preferred for mapping purposes. Coding sequences are more likely to be
10 conserved within gene families, thus increasing the chance of cross hybridizations during chromosomal mapping.

Once a sequence has been mapped to a precise chromosomal location, the physical position of the sequence on the chromosome can be correlated with genetic map data. Such data are found, *e.g.*, in McKusick, MENDELIAN INHERITANCE IN MAN, available on-line through
15 Johns Hopkins University Welch Medical Library). The relationship between genes and disease, mapped to the same chromosomal region, can then be identified through linkage analysis (co-inheritance of physically adjacent genes), described in, *e.g.*, Egeland, *et al.*, 1987. *Nature*, 325: 783-787.

Moreover, differences in the DNA sequences between individuals affected and
20 unaffected with a disease associated with the NOVX gene, can be determined. If a mutation is observed in some or all of the affected individuals but not in any unaffected individuals, then the mutation is likely to be the causative agent of the particular disease. Comparison of affected and unaffected individuals generally involves first looking for structural alterations in the chromosomes, such as deletions or translocations that are visible from chromosome spreads or
25 detectable using PCR based on that DNA sequence. Ultimately, complete sequencing of genes from several individuals can be performed to confirm the presence of a mutation and to distinguish mutations from polymorphisms.

Tissue Typing

30 The NOVX sequences of the invention can also be used to identify individuals from minute biological samples. In this technique, an individual's genomic DNA is digested with one or more restriction enzymes, and probed on a Southern blot to yield unique bands for

identification. The sequences of the invention are useful as additional DNA markers for RFLP ("restriction fragment length polymorphisms," described in U.S. Patent No. 5,272,057).

Furthermore, the sequences of the invention can be used to provide an alternative technique that determines the actual base-by-base DNA sequence of selected portions of an individual's genome. Thus, the NOVX sequences described herein can be used to prepare two PCR primers from the 5'- and 3'-termini of the sequences. These primers can then be used to amplify an individual's DNA and subsequently sequence it.

Panels of corresponding DNA sequences from individuals, prepared in this manner, can provide unique individual identifications, as each individual will have a unique set of such DNA sequences due to allelic differences. The sequences of the invention can be used to obtain such identification sequences from individuals and from tissue. The NOVX sequences of the invention uniquely represent portions of the human genome. Allelic variation occurs to some degree in the coding regions of these sequences, and to a greater degree in the noncoding regions. It is estimated that allelic variation between individual humans occurs with a frequency of about once per each 500 bases. Much of the allelic variation is due to single nucleotide polymorphisms (SNPs), which include restriction fragment length polymorphisms (RFLPs).

Each of the sequences described herein can, to some degree, be used as a standard against which DNA from an individual can be compared for identification purposes. Because greater numbers of polymorphisms occur in the noncoding regions, fewer sequences are necessary to differentiate individuals. The noncoding sequences can comfortably provide positive individual identification with a panel of perhaps 10 to 1,000 primers that each yield a noncoding amplified sequence of 100 bases. If predicted coding sequences, such as those in SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, or 33 are used, a more appropriate number of primers for positive individual identification would be 500-2,000.

Predictive Medicine

The invention also pertains to the field of predictive medicine in which diagnostic assays, prognostic assays, pharmacogenomics, and monitoring clinical trials are used for prognostic (predictive) purposes to thereby treat an individual prophylactically. Accordingly, one aspect of the invention relates to diagnostic assays for determining NOVX protein and/or nucleic acid expression as well as NOVX activity, in the context of a biological sample (*e.g.*,

blood, serum, cells, tissue) to thereby determine whether an individual is afflicted with a disease or disorder, or is at risk of developing a disorder, associated with aberrant NOVX expression or activity. The disorders include metabolic disorders, diabetes, obesity, infectious disease, anorexia, cancer-associated cachexia, cancer, neurodegenerative disorders, Alzheimer's
5 Disease, Parkinson's Disorder, immune disorders, and hematopoietic disorders, and the various dyslipidemias, metabolic disturbances associated with obesity, the metabolic syndrome X and wasting disorders associated with chronic diseases and various cancers. The invention also provides for prognostic (or predictive) assays for determining whether an individual is at risk of developing a disorder associated with NOVX protein, nucleic acid expression or activity. For
10 example, mutations in an NOVX gene can be assayed in a biological sample. Such assays can be used for prognostic or predictive purpose to thereby prophylactically treat an individual prior to the onset of a disorder characterized by or associated with NOVX protein, nucleic acid expression, or biological activity.

Another aspect of the invention provides methods for determining NOVX protein,
15 nucleic acid expression or activity in an individual to thereby select appropriate therapeutic or prophylactic agents for that individual (referred to herein as "pharmacogenomics"). Pharmacogenomics allows for the selection of agents (*e.g.*, drugs) for therapeutic or prophylactic treatment of an individual based on the genotype of the individual (*e.g.*, the genotype of the individual examined to determine the ability of the individual to respond to a
20 particular agent.)

Yet another aspect of the invention pertains to monitoring the influence of agents (*e.g.*, drugs, compounds) on the expression or activity of NOVX in clinical trials.

These and other agents are described in further detail in the following sections.

25 **Diagnostic Assays**

An exemplary method for detecting the presence or absence of NOVX in a biological sample involves obtaining a biological sample from a test subject and contacting the biological sample with a compound or an agent capable of detecting NOVX protein or nucleic acid (*e.g.*, mRNA, genomic DNA) that encodes NOVX protein such that the presence of NOVX is
30 detected in the biological sample. An agent for detecting NOVX mRNA or genomic DNA is a labeled nucleic acid probe capable of hybridizing to NOVX mRNA or genomic DNA. The nucleic acid probe can be, for example, a full-length NOVX nucleic acid, such as the nucleic

acid of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, or 33, or a portion thereof, such as an oligonucleotide of at least 15, 30, 50, 100, 250 or 500 nucleotides in length and sufficient to specifically hybridize under stringent conditions to NOVX mRNA or genomic DNA. Other suitable probes for use in the diagnostic assays of the invention are described
5 herein.

An agent for detecting NOVX protein is an antibody capable of binding to NOVX protein, preferably an antibody with a detectable label. Antibodies can be polyclonal, or more preferably, monoclonal. An intact antibody, or a fragment thereof (*e.g.*, Fab or F(ab')₂) can be used. The term "labeled", with regard to the probe or antibody, is intended to encompass direct
10 labeling of the probe or antibody by coupling (*i.e.*, physically linking) a detectable substance to the probe or antibody, as well as indirect labeling of the probe or antibody by reactivity with another reagent that is directly labeled. Examples of indirect labeling include detection of a primary antibody using a fluorescently-labeled secondary antibody and end-labeling of a DNA probe with biotin such that it can be detected with fluorescently-labeled streptavidin. The term
15 "biological sample" is intended to include tissues, cells and biological fluids isolated from a subject, as well as tissues, cells and fluids present within a subject. That is, the detection method of the invention can be used to detect NOVX mRNA, protein, or genomic DNA in a biological sample *in vitro* as well as *in vivo*. For example, *in vitro* techniques for detection of NOVX mRNA include Northern hybridizations and *in situ* hybridizations. *In vitro* techniques
20 for detection of NOVX protein include enzyme linked immunosorbent assays (ELISAs), Western blots, immunoprecipitations, and immunofluorescence. *In vitro* techniques for detection of NOVX genomic DNA include Southern hybridizations. Furthermore, *in vivo* techniques for detection of NOVX protein include introducing into a subject a labeled anti-NOVX antibody. For example, the antibody can be labeled with a radioactive marker
25 whose presence and location in a subject can be detected by standard imaging techniques.

In one embodiment, the biological sample contains protein molecules from the test subject. Alternatively, the biological sample can contain mRNA molecules from the test subject or genomic DNA molecules from the test subject. A preferred biological sample is a peripheral blood leukocyte sample isolated by conventional means from a subject.

30 In another embodiment, the methods further involve obtaining a control biological sample from a control subject, contacting the control sample with a compound or agent capable of detecting NOVX protein, mRNA, or genomic DNA, such that the presence of NOVX

protein, mRNA or genomic DNA is detected in the biological sample, and comparing the presence of NOVX protein, mRNA or genomic DNA in the control sample with the presence of NOVX protein, mRNA or genomic DNA in the test sample.

The invention also encompasses kits for detecting the presence of NOVX in a biological sample. For example, the kit can comprise: a labeled compound or agent capable of detecting NOVX protein or mRNA in a biological sample; means for determining the amount of NOVX in the sample; and means for comparing the amount of NOVX in the sample with a standard. The compound or agent can be packaged in a suitable container. The kit can further comprise instructions for using the kit to detect NOVX protein or nucleic acid.

Prognostic Assays

The diagnostic methods described herein can furthermore be utilized to identify subjects having or at risk of developing a disease or disorder associated with aberrant NOVX expression or activity. For example, the assays described herein, such as the preceding diagnostic assays or the following assays, can be utilized to identify a subject having or at risk of developing a disorder associated with NOVX protein, nucleic acid expression or activity. Alternatively, the prognostic assays can be utilized to identify a subject having or at risk for developing a disease or disorder. Thus, the invention provides a method for identifying a disease or disorder associated with aberrant NOVX expression or activity in which a test sample is obtained from a subject and NOVX protein or nucleic acid (*e.g.*, mRNA, genomic DNA) is detected, wherein the presence of NOVX protein or nucleic acid is diagnostic for a subject having or at risk of developing a disease or disorder associated with aberrant NOVX expression or activity. As used herein, a "test sample" refers to a biological sample obtained from a subject of interest. For example, a test sample can be a biological fluid (*e.g.*, serum), cell sample, or tissue.

Furthermore, the prognostic assays described herein can be used to determine whether a subject can be administered an agent (*e.g.*, an agonist, antagonist, peptidomimetic, protein, peptide, nucleic acid, small molecule, or other drug candidate) to treat a disease or disorder associated with aberrant NOVX expression or activity. For example, such methods can be used to determine whether a subject can be effectively treated with an agent for a disorder. Thus, the invention provides methods for determining whether a subject can be effectively treated with an agent for a disorder associated with aberrant NOVX expression or activity in which a test sample is obtained and NOVX protein or nucleic acid is detected (*e.g.*, wherein the presence of

NOVX protein or nucleic acid is diagnostic for a subject that can be administered the agent to treat a disorder associated with aberrant NOVX expression or activity).

The methods of the invention can also be used to detect genetic lesions in an NOVX gene, thereby determining if a subject with the lesioned gene is at risk for a disorder characterized by aberrant cell proliferation and/or differentiation. In various embodiments, the methods include detecting, in a sample of cells from the subject, the presence or absence of a genetic lesion characterized by at least one of an alteration affecting the integrity of a gene encoding an NOVX-protein, or the misexpression of the NOVX gene. For example, such genetic lesions can be detected by ascertaining the existence of at least one of: (i) a deletion of one or more nucleotides from an NOVX gene; (ii) an addition of one or more nucleotides to an NOVX gene; (iii) a substitution of one or more nucleotides of an NOVX gene, (iv) a chromosomal rearrangement of an NOVX gene; (v) an alteration in the level of a messenger RNA transcript of an NOVX gene, (vi) aberrant modification of an NOVX gene, such as of the methylation pattern of the genomic DNA, (vii) the presence of a non-wild-type splicing pattern of a messenger RNA transcript of an NOVX gene, (viii) a non-wild-type level of an NOVX protein, (ix) allelic loss of an NOVX gene, and (x) inappropriate post-translational modification of an NOVX protein. As described herein, there are a large number of assay techniques known in the art which can be used for detecting lesions in an NOVX gene. A preferred biological sample is a peripheral blood leukocyte sample isolated by conventional means from a subject. However, any biological sample containing nucleated cells may be used, including, for example, buccal mucosal cells.

In certain embodiments, detection of the lesion involves the use of a probe/primer in a polymerase chain reaction (PCR) (*see, e.g.,* U.S. Patent Nos. 4,683,195 and 4,683,202), such as anchor PCR or RACE PCR, or, alternatively, in a ligation chain reaction (LCR) (*see, e.g.,* Landegran, *et al.*, 1988. *Science* 241: 1077-1080; and Nakazawa, *et al.*, 1994. *Proc. Natl. Acad. Sci. USA* 91: 360-364), the latter of which can be particularly useful for detecting point mutations in the NOVX-gene (*see, Abravaya, et al.*, 1995. *Nucl. Acids Res.* 23: 675-682). This method can include the steps of collecting a sample of cells from a patient, isolating nucleic acid (*e.g.,* genomic, mRNA or both) from the cells of the sample, contacting the nucleic acid sample with one or more primers that specifically hybridize to an NOVX gene under conditions such that hybridization and amplification of the NOVX gene (if present) occurs, and detecting the presence or absence of an amplification product, or detecting the size of the amplification

product and comparing the length to a control sample. It is anticipated that PCR and/or LCR may be desirable to use as a preliminary amplification step in conjunction with any of the techniques used for detecting mutations described herein.

Alternative amplification methods include: self sustained sequence replication (*see*,
5 Guatelli, *et al.*, 1990. *Proc. Natl. Acad. Sci. USA* 87: 1874-1878), transcriptional amplification system (*see*, Kwoh, *et al.*, 1989. *Proc. Natl. Acad. Sci. USA* 86: 1173-1177); Q β Replicase (*see*, Lizardi, *et al.*, 1988. *BioTechnology* 6: 1197), or any other nucleic acid amplification method, followed by the detection of the amplified molecules using techniques well known to those of skill in the art. These detection schemes are especially useful for the detection of nucleic acid
10 molecules if such molecules are present in very low numbers.

In an alternative embodiment, mutations in an NOVX gene from a sample cell can be identified by alterations in restriction enzyme cleavage patterns. For example, sample and control DNA is isolated, amplified (optionally), digested with one or more restriction endonucleases, and fragment length sizes are determined by gel electrophoresis and compared.
15 Differences in fragment length sizes between sample and control DNA indicates mutations in the sample DNA. Moreover, the use of sequence specific ribozymes (*see, e.g.*, U.S. Patent No. 5,493,531) can be used to score for the presence of specific mutations by development or loss of a ribozyme cleavage site.

In other embodiments, genetic mutations in NOVX can be identified by hybridizing a
20 sample and control nucleic acids, *e.g.*, DNA or RNA, to high-density arrays containing hundreds or thousands of oligonucleotides probes. *See, e.g.*, Cronin, *et al.*, 1996. *Human Mutation* 7: 244-255; Kozal, *et al.*, 1996. *Nat. Med.* 2: 753-759. For example, genetic mutations in NOVX can be identified in two dimensional arrays containing light-generated DNA probes as described in Cronin, *et al.*, *supra*. Briefly, a first hybridization array of probes
25 can be used to scan through long stretches of DNA in a sample and control to identify base changes between the sequences by making linear arrays of sequential overlapping probes. This step allows the identification of point mutations. This is followed by a second hybridization array that allows the characterization of specific mutations by using smaller, specialized probe arrays complementary to all variants or mutations detected. Each mutation array is composed
30 of parallel probe sets, one complementary to the wild-type gene and the other complementary to the mutant gene.

In yet another embodiment, any of a variety of sequencing reactions known in the art can be used to directly sequence the NOVX gene and detect mutations by comparing the sequence of the sample NOVX with the corresponding wild-type (control) sequence. Examples of sequencing reactions include those based on techniques developed by Maxim and Gilbert, 1977. *Proc. Natl. Acad. Sci. USA* 74: 560 or Sanger, 1977. *Proc. Natl. Acad. Sci. USA* 74: 5463. It is also contemplated that any of a variety of automated sequencing procedures can be utilized when performing the diagnostic assays (see, e.g., Naeve, *et al.*, 1995. *Biotechniques* 19: 448), including sequencing by mass spectrometry (see, e.g., PCT International Publication No. WO 94/16101; Cohen, *et al.*, 1996. *Adv. Chromatography* 36: 127-162; and Griffin, *et al.*, 1993. *Appl. Biochem. Biotechnol.* 38: 147-159).

Other methods for detecting mutations in the NOVX gene include methods in which protection from cleavage agents is used to detect mismatched bases in RNA/RNA or RNA/DNA heteroduplexes. See, e.g., Myers, *et al.*, 1985. *Science* 230: 1242. In general, the art technique of "mismatch cleavage" starts by providing heteroduplexes of formed by hybridizing (labeled) RNA or DNA containing the wild-type NOVX sequence with potentially mutant RNA or DNA obtained from a tissue sample. The double-stranded duplexes are treated with an agent that cleaves single-stranded regions of the duplex such as which will exist due to basepair mismatches between the control and sample strands. For instance, RNA/DNA duplexes can be treated with RNase and DNA/DNA hybrids treated with S₁ nuclease to enzymatically digesting the mismatched regions. In other embodiments, either DNA/DNA or RNA/DNA duplexes can be treated with hydroxylamine or osmium tetroxide and with piperidine in order to digest mismatched regions. After digestion of the mismatched regions, the resulting material is then separated by size on denaturing polyacrylamide gels to determine the site of mutation. See, e.g., Cotton, *et al.*, 1988. *Proc. Natl. Acad. Sci. USA* 85: 4397; Saleeba, *et al.*, 1992. *Methods Enzymol.* 217: 286-295. In an embodiment, the control DNA or RNA can be labeled for detection.

In still another embodiment, the mismatch cleavage reaction employs one or more proteins that recognize mismatched base pairs in double-stranded DNA (so called "DNA mismatch repair" enzymes) in defined systems for detecting and mapping point mutations in NOVX cDNAs obtained from samples of cells. For example, the mutY enzyme of *E. coli* cleaves A at G/A mismatches and the thymidine DNA glycosylase from HeLa cells cleaves T at G/T mismatches. See, e.g., Hsu, *et al.*, 1994. *Carcinogenesis* 15: 1657-1662. According to an

exemplary embodiment, a probe based on an NOVX sequence, *e.g.*, a wild-type NOVX sequence, is hybridized to a cDNA or other DNA product from a test cell(s). The duplex is treated with a DNA mismatch repair enzyme, and the cleavage products, if any, can be detected from electrophoresis protocols or the like. *See, e.g.*, U.S. Patent No. 5,459,039.

5 In other embodiments, alterations in electrophoretic mobility will be used to identify mutations in NOVX genes. For example, single strand conformation polymorphism (SSCP) may be used to detect differences in electrophoretic mobility between mutant and wild type nucleic acids. *See, e.g.*, Orita, *et al.*, 1989. *Proc. Natl. Acad. Sci. USA*: 86: 2766; Cotton, 1993. *Mutat. Res.* 285: 125-144; Hayashi, 1992. *Genet. Anal. Tech. Appl.* 9: 73-79. Single-stranded
10 DNA fragments of sample and control NOVX nucleic acids will be denatured and allowed to renature. The secondary structure of single-stranded nucleic acids varies according to sequence, the resulting alteration in electrophoretic mobility enables the detection of even a single base change. The DNA fragments may be labeled or detected with labeled probes. The sensitivity of the assay may be enhanced by using RNA (rather than DNA), in which the
15 secondary structure is more sensitive to a change in sequence. In one embodiment, the subject method utilizes heteroduplex analysis to separate double stranded heteroduplex molecules on the basis of changes in electrophoretic mobility. *See, e.g.*, Keen, *et al.*, 1991. *Trends Genet.* 7: 5.

In yet another embodiment, the movement of mutant or wild-type fragments in
20 polyacrylamide gels containing a gradient of denaturant is assayed using denaturing gradient gel electrophoresis (DGGE). *See, e.g.*, Myers, *et al.*, 1985. *Nature* 313: 495. When DGGE is used as the method of analysis, DNA will be modified to insure that it does not completely denature, for example by adding a GC clamp of approximately 40 bp of high-melting GC-rich DNA by PCR. In a further embodiment, a temperature gradient is used in place of a denaturing
25 gradient to identify differences in the mobility of control and sample DNA. *See, e.g.*, Rosenbaum and Reissner, 1987. *Biophys. Chem.* 265: 12753.

Examples of other techniques for detecting point mutations include, but are not limited to, selective oligonucleotide hybridization, selective amplification, or selective primer
30 extension. For example, oligonucleotide primers may be prepared in which the known mutation is placed centrally and then hybridized to target DNA under conditions that permit hybridization only if a perfect match is found. *See, e.g.*, Saiki, *et al.*, 1986. *Nature* 324: 163; Saiki, *et al.*, 1989. *Proc. Natl. Acad. Sci. USA* 86: 6230. Such allele specific oligonucleotides

are hybridized to PCR amplified target DNA or a number of different mutations when the oligonucleotides are attached to the hybridizing membrane and hybridized with labeled target DNA.

Alternatively, allele specific amplification technology that depends on selective PCR amplification may be used in conjunction with the instant invention. Oligonucleotides used as primers for specific amplification may carry the mutation of interest in the center of the molecule (so that amplification depends on differential hybridization; *see, e.g.,* Gibbs, *et al.*, 1989. *Nucl. Acids Res.* 17: 2437-2448) or at the extreme 3'-terminus of one primer where, under appropriate conditions, mismatch can prevent, or reduce polymerase extension (*see, e.g.,* Prossner, 1993. *Tibtech.* 11: 238). In addition it may be desirable to introduce a novel restriction site in the region of the mutation to create cleavage-based detection. *See, e.g.,* Gasparini, *et al.*, 1992. *Mol. Cell Probes* 6: 1. It is anticipated that in certain embodiments amplification may also be performed using *Taq* ligase for amplification. *See, e.g.,* Barany, 1991. *Proc. Natl. Acad. Sci. USA* 88: 189. In such cases, ligation will occur only if there is a perfect match at the 3'-terminus of the 5' sequence, making it possible to detect the presence of a known mutation at a specific site by looking for the presence or absence of amplification.

The methods described herein may be performed, for example, by utilizing pre-packaged diagnostic kits comprising at least one probe nucleic acid or antibody reagent described herein, which may be conveniently used, *e.g.,* in clinical settings to diagnose patients exhibiting symptoms or family history of a disease or illness involving an NOVX gene.

Furthermore, any cell type or tissue, preferably peripheral blood leukocytes, in which NOVX is expressed may be utilized in the prognostic assays described herein. However, any biological sample containing nucleated cells may be used, including, for example, buccal mucosal cells.

Pharmacogenomics

Agents, or modulators that have a stimulatory or inhibitory effect on NOVX activity (*e.g.,* NOVX gene expression), as identified by a screening assay described herein can be administered to individuals to treat (prophylactically or therapeutically) disorders (The disorders include metabolic disorders, diabetes, obesity, infectious disease, anorexia, cancer-associated cachexia, cancer, neurodegenerative disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders, and hematopoietic disorders, and the various dyslipidemias,

metabolic disturbances associated with obesity, the metabolic syndrome X and wasting disorders associated with chronic diseases and various cancers.) In conjunction with such treatment, the pharmacogenomics (*i.e.*, the study of the relationship between an individual's genotype and that individual's response to a foreign compound or drug) of the individual may be considered. Differences in metabolism of therapeutics can lead to severe toxicity or therapeutic failure by altering the relation between dose and blood concentration of the pharmacologically active drug. Thus, the pharmacogenomics of the individual permits the selection of effective agents (*e.g.*, drugs) for prophylactic or therapeutic treatments based on a consideration of the individual's genotype. Such pharmacogenomics can further be used to determine appropriate dosages and therapeutic regimens. Accordingly, the activity of NOVX protein, expression of NOVX nucleic acid, or mutation content of NOVX genes in an individual can be determined to thereby select appropriate agent(s) for therapeutic or prophylactic treatment of the individual.

Pharmacogenomics deals with clinically significant hereditary variations in the response to drugs due to altered drug disposition and abnormal action in affected persons. See *e.g.*, Eichelbaum, 1996. *Clin. Exp. Pharmacol. Physiol.*, 23: 983-985; Linder, 1997. *Clin. Chem.*, 43: 254-266. In general, two types of pharmacogenetic conditions can be differentiated. Genetic conditions transmitted as a single factor altering the way drugs act on the body (altered drug action) or genetic conditions transmitted as single factors altering the way the body acts on drugs (altered drug metabolism). These pharmacogenetic conditions can occur either as rare defects or as polymorphisms. For example, glucose-6-phosphate dehydrogenase (G6PD) deficiency is a common inherited enzymopathy in which the main clinical complication is hemolysis after ingestion of oxidant drugs (anti-malarials, sulfonamides, analgesics, nitrofurans) and consumption of fava beans.

As an illustrative embodiment, the activity of drug metabolizing enzymes is a major determinant of both the intensity and duration of drug action. The discovery of genetic polymorphisms of drug metabolizing enzymes (*e.g.*, N-acetyltransferase 2 (NAT 2) and cytochrome P450 enzymes CYP2D6 and CYP2C19) has provided an explanation as to why some patients do not obtain the expected drug effects or show exaggerated drug response and serious toxicity after taking the standard and safe dose of a drug. These polymorphisms are expressed in two phenotypes in the population, the extensive metabolizer (EM) and poor metabolizer (PM). The prevalence of PM is different among different populations. For

example, the gene coding for CYP2D6 is highly polymorphic and several mutations have been identified in PM, which all lead to the absence of functional CYP2D6. Poor metabolizers of CYP2D6 and CYP2C19 quite frequently experience exaggerated drug response and side effects when they receive standard doses. If a metabolite is the active therapeutic moiety, PM show no therapeutic response, as demonstrated for the analgesic effect of codeine mediated by its CYP2D6-formed metabolite morphine. At the other extreme are the so called ultra-rapid metabolizers who do not respond to standard doses. Recently, the molecular basis of ultra-rapid metabolism has been identified to be due to CYP2D6 gene amplification.

Thus, the activity of NOVX protein, expression of NOVX nucleic acid, or mutation content of NOVX genes in an individual can be determined to thereby select appropriate agent(s) for therapeutic or prophylactic treatment of the individual. In addition, pharmacogenetic studies can be used to apply genotyping of polymorphic alleles encoding drug-metabolizing enzymes to the identification of an individual's drug responsiveness phenotype. This knowledge, when applied to dosing or drug selection, can avoid adverse reactions or therapeutic failure and thus enhance therapeutic or prophylactic efficiency when treating a subject with an NOVX modulator, such as a modulator identified by one of the exemplary screening assays described herein.

Monitoring of Effects During Clinical Trials

Monitoring the influence of agents (*e.g.*, drugs, compounds) on the expression or activity of NOVX (*e.g.*, the ability to modulate aberrant cell proliferation and/or differentiation) can be applied not only in basic drug screening, but also in clinical trials. For example, the effectiveness of an agent determined by a screening assay as described herein to increase NOVX gene expression, protein levels, or upregulate NOVX activity, can be monitored in clinical trials of subjects exhibiting decreased NOVX gene expression, protein levels, or downregulated NOVX activity. Alternatively, the effectiveness of an agent determined by a screening assay to decrease NOVX gene expression, protein levels, or downregulate NOVX activity, can be monitored in clinical trials of subjects exhibiting increased NOVX gene expression, protein levels, or upregulated NOVX activity. In such clinical trials, the expression or activity of NOVX and, preferably, other genes that have been implicated in, for example, a cellular proliferation or immune disorder can be used as a "read out" or markers of the immune responsiveness of a particular cell.

By way of example, and not of limitation, genes, including NOVX, that are modulated in cells by treatment with an agent (*e.g.*, compound, drug or small molecule) that modulates NOVX activity (*e.g.*, identified in a screening assay as described herein) can be identified. Thus, to study the effect of agents on cellular proliferation disorders, for example, in a clinical trial, cells can be isolated and RNA prepared and analyzed for the levels of expression of NOVX and other genes implicated in the disorder. The levels of gene expression (*i.e.*, a gene expression pattern) can be quantified by Northern blot analysis or RT-PCR, as described herein, or alternatively by measuring the amount of protein produced, by one of the methods as described herein, or by measuring the levels of activity of NOVX or other genes. In this manner, the gene expression pattern can serve as a marker, indicative of the physiological response of the cells to the agent. Accordingly, this response state may be determined before, and at various points during, treatment of the individual with the agent.

In one embodiment, the invention provides a method for monitoring the effectiveness of treatment of a subject with an agent (*e.g.*, an agonist, antagonist, protein, peptide, peptidomimetic, nucleic acid, small molecule, or other drug candidate identified by the screening assays described herein) comprising the steps of (i) obtaining a pre-administration sample from a subject prior to administration of the agent; (ii) detecting the level of expression of an NOVX protein, mRNA, or genomic DNA in the preadministration sample; (iii) obtaining one or more post-administration samples from the subject; (iv) detecting the level of expression or activity of the NOVX protein, mRNA, or genomic DNA in the post-administration samples; (v) comparing the level of expression or activity of the NOVX protein, mRNA, or genomic DNA in the pre-administration sample with the NOVX protein, mRNA, or genomic DNA in the post administration sample or samples; and (vi) altering the administration of the agent to the subject accordingly. For example, increased administration of the agent may be desirable to increase the expression or activity of NOVX to higher levels than detected, *i.e.*, to increase the effectiveness of the agent. Alternatively, decreased administration of the agent may be desirable to decrease expression or activity of NOVX to lower levels than detected, *i.e.*, to decrease the effectiveness of the agent.

Methods of Treatment

The invention provides for both prophylactic and therapeutic methods of treating a subject at risk of (or susceptible to) a disorder or having a disorder associated with aberrant

NOVX expression or activity. The disorders include cardiomyopathy, atherosclerosis, hypertension, congenital heart defects, aortic stenosis, atrial septal defect (ASD), atrioventricular (A-V) canal defect, ductus arteriosus, pulmonary stenosis, subaortic stenosis, ventricular septal defect (VSD), valve diseases, tuberous sclerosis, scleroderma, obesity, transplantation, adrenoleukodystrophy, congenital adrenal hyperplasia, prostate cancer, neoplasm; adenocarcinoma, lymphoma, uterus cancer, fertility, hemophilia, hypercoagulation, idiopathic thrombocytopenic purpura, immunodeficiencies, graft versus host disease, AIDS, bronchial asthma, Crohn's disease; multiple sclerosis, treatment of Albright Hereditary Osteodystrophy, and other diseases, disorders and conditions of the like.

These methods of treatment will be discussed more fully, below.

Disease and Disorders

Diseases and disorders that are characterized by increased (relative to a subject not suffering from the disease or disorder) levels or biological activity may be treated with Therapeutics that antagonize (*i.e.*, reduce or inhibit) activity. Therapeutics that antagonize activity may be administered in a therapeutic or prophylactic manner. Therapeutics that may be utilized include, but are not limited to: (i) an aforementioned peptide, or analogs, derivatives, fragments or homologs thereof; (ii) antibodies to an aforementioned peptide; (iii) nucleic acids encoding an aforementioned peptide; (iv) administration of antisense nucleic acid and nucleic acids that are "dysfunctional" (*i.e.*, due to a heterologous insertion within the coding sequences of coding sequences to an aforementioned peptide) that are utilized to "knockout" endogenous function of an aforementioned peptide by homologous recombination (*see, e.g.*, Capecchi, 1989. *Science* 244: 1288-1292); or (v) modulators (*i.e.*, inhibitors, agonists and antagonists, including additional peptide mimetic of the invention or antibodies specific to a peptide of the invention) that alter the interaction between an aforementioned peptide and its binding partner.

Diseases and disorders that are characterized by decreased (relative to a subject not suffering from the disease or disorder) levels or biological activity may be treated with Therapeutics that increase (*i.e.*, are agonists to) activity. Therapeutics that upregulate activity may be administered in a therapeutic or prophylactic manner. Therapeutics that may be utilized include, but are not limited to, an aforementioned peptide, or analogs, derivatives, fragments or homologs thereof; or an agonist that increases bioavailability.

Increased or decreased levels can be readily detected by quantifying peptide and/or RNA, by obtaining a patient tissue sample (*e.g.*, from biopsy tissue) and assaying it *in vitro* for RNA or peptide levels, structure and/or activity of the expressed peptides (or mRNAs of an aforementioned peptide). Methods that are well-known within the art include, but are not
5 limited to, immunoassays (*e.g.*, by Western blot analysis, immunoprecipitation followed by sodium dodecyl sulfate (SDS) polyacrylamide gel electrophoresis, immunocytochemistry, etc.) and/or hybridization assays to detect expression of mRNAs (*e.g.*, Northern assays, dot blots, *in situ* hybridization, and the like).

10 Prophylactic Methods

In one aspect, the invention provides a method for preventing, in a subject, a disease or condition associated with an aberrant NOVX expression or activity, by administering to the subject an agent that modulates NOVX expression or at least one NOVX activity. Subjects at risk for a disease that is caused or contributed to by aberrant NOVX expression or activity can
15 be identified by, for example, any or a combination of diagnostic or prognostic assays as described herein. Administration of a prophylactic agent can occur prior to the manifestation of symptoms characteristic of the NOVX aberrancy, such that a disease or disorder is prevented or, alternatively, delayed in its progression. Depending upon the type of NOVX aberrancy, for example, an NOVX agonist or NOVX antagonist agent can be used for treating the subject.
20 The appropriate agent can be determined based on screening assays described herein. The prophylactic methods of the invention are further discussed in the following subsections.

Therapeutic Methods

Another aspect of the invention pertains to methods of modulating NOVX expression or
25 activity for therapeutic purposes. The modulatory method of the invention involves contacting a cell with an agent that modulates one or more of the activities of NOVX protein activity associated with the cell. An agent that modulates NOVX protein activity can be an agent as described herein, such as a nucleic acid or a protein, a naturally-occurring cognate ligand of an NOVX protein, a peptide, an NOVX peptidomimetic, or other small molecule. In one
30 embodiment, the agent stimulates one or more NOVX protein activity. Examples of such stimulatory agents include active NOVX protein and a nucleic acid molecule encoding NOVX that has been introduced into the cell. In another embodiment, the agent inhibits one or more

NOVX protein activity. Examples of such inhibitory agents include antisense NOVX nucleic acid molecules and anti-NOVX antibodies. These modulatory methods can be performed *in vitro* (e.g., by culturing the cell with the agent) or, alternatively, *in vivo* (e.g., by administering the agent to a subject). As such, the invention provides methods of treating an individual
5 afflicted with a disease or disorder characterized by aberrant expression or activity of an NOVX protein or nucleic acid molecule. In one embodiment, the method involves administering an agent (e.g., an agent identified by a screening assay described herein), or combination of agents that modulates (e.g., up-regulates or down-regulates) NOVX expression or activity. In another embodiment, the method involves administering an NOVX protein or nucleic acid molecule as
10 therapy to compensate for reduced or aberrant NOVX expression or activity.

Stimulation of NOVX activity is desirable *in situations* in which NOVX is abnormally downregulated and/or in which increased NOVX activity is likely to have a beneficial effect. One example of such a situation is where a subject has a disorder characterized by aberrant cell proliferation and/or differentiation (e.g., cancer or immune associated disorders). Another
15 example of such a situation is where the subject has a gestational disease (e.g., preeclampsia).

Determination of the Biological Effect of the Therapeutic

In various embodiments of the invention, suitable *in vitro* or *in vivo* assays are performed to determine the effect of a specific Therapeutic and whether its administration is indicated for treatment of the affected tissue.

20 In various specific embodiments, *in vitro* assays may be performed with representative cells of the type(s) involved in the patient's disorder, to determine if a given Therapeutic exerts the desired effect upon the cell type(s). Compounds for use in therapy may be tested in suitable animal model systems including, but not limited to rats, mice, chicken, cows, monkeys, rabbits, and the like, prior to testing in human subjects. Similarly, for *in vivo* testing, any of the animal
25 model system known in the art may be used prior to administration to human subjects.

Prophylactic and Therapeutic Uses of the Compositions of the Invention

The NOVX nucleic acids and proteins of the invention are useful in potential prophylactic and therapeutic applications implicated in a variety of disorders including, but not limited to: metabolic disorders, diabetes, obesity, infectious disease, anorexia, cancer-associated
30 cancer, neurodegenerative disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders, hematopoietic disorders, and the various dyslipidemias, metabolic disturbances

associated with obesity, the metabolic syndrome X and wasting disorders associated with chronic diseases and various cancers.

As an example, a cDNA encoding the NOVX protein of the invention may be useful in gene therapy, and the protein may be useful when administered to a subject in need thereof. By way of non-limiting example, the compositions of the invention will have efficacy for treatment of patients suffering from: metabolic disorders, diabetes, obesity, infectious disease, anorexia, cancer-associated cachexia, cancer, neurodegenerative disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders, hematopoietic disorders, and the various dyslipidemias.

Both the novel nucleic acid encoding the NOVX protein, and the NOVX protein of the invention, or fragments thereof, may also be useful in diagnostic applications, wherein the presence or amount of the nucleic acid or the protein are to be assessed. A further use could be as an anti-bacterial molecule (*i.e.*, some peptides have been found to possess anti-bacterial properties). These materials are further useful in the generation of antibodies, which immunospecifically-bind to the novel substances of the invention for use in therapeutic or diagnostic methods.

The invention will be further described in the following examples, which do not limit the scope of the invention described in the claims.

Example 1. Quantitative expression analysis of clones in various cells and tissues

The quantitative expression of various clones was assessed using microtiter plates containing RNA samples from a variety of normal and pathology-derived cells, cell lines and tissues using real time quantitative PCR (RTQ PCR; TAQMAN[®]). RTQ PCR was performed on a Perkin-Elmer Biosystems ABI PRISM[®] 7700 Sequence Detection System. Various collections of samples are assembled on the plates, and referred to as Panel 1 (containing cells and cell lines from normal and cancer sources), Panel 2 (containing samples derived from tissues, in particular from surgical samples, from normal and cancer sources), Panel 3 (containing samples derived from a wide variety of cancer sources) and Panel 4 (containing cells and cell lines from normal cells and cells related to inflammatory conditions).

First, the RNA samples were normalized to constitutively expressed genes such as β -actin and GAPDH. RNA (~50 ng total or ~1 ng polyA+) was converted to cDNA using the

TAQMAN[®] Reverse Transcription Reagents Kit (PE Biosystems, Foster City, CA; Catalog No. N808-0234) and random hexamers according to the manufacturer's protocol. Reactions were performed in 20 ul and incubated for 30 min. at 48⁰C. cDNA (5 ul) was then transferred to a separate plate for the TAQMAN[®] reaction using β -actin and GAPDH TAQMAN[®] Assay Reagents (PE Biosystems; Catalog Nos. 4310881E and 4310884E, respectively) and TAQMAN[®] universal PCR Master Mix (PE Biosystems; Catalog No. 4304447) according to the manufacturer's protocol. Reactions were performed in 25 ul using the following parameters: 2 min. at 50⁰C; 10 min. at 95⁰C; 15 sec. at 95⁰C/1 min. at 60⁰C (40 cycles). Results were recorded as CT values (cycle at which a given sample crosses a threshold level of fluorescence) using a log scale, with the difference in RNA concentration between a given sample and the sample with the lowest CT value being represented as 2 to the power of delta CT. The percent relative expression is then obtained by taking the reciprocal of this RNA difference and multiplying by 100. The average CT values obtained for β -actin and GAPDH were used to normalize RNA samples. The RNA sample generating the highest CT value required no further diluting, while all other samples were diluted relative to this sample according to their β -actin /GAPDH average CT values.

Normalized RNA (5 ul) was converted to cDNA and analyzed via TAQMAN[®] using One Step RT-PCR Master Mix Reagents (PE Biosystems; Catalog No. 4309169) and gene-specific primers according to the manufacturer's instructions. Probes and primers were designed for each assay according to Perkin Elmer Biosystem's *Primer Express* Software package (version I for Apple Computer's Macintosh Power PC) or a similar algorithm using the target sequence as input. Default settings were used for reaction conditions and the following parameters were set before selecting primers: primer concentration = 250 nM, primer melting temperature (T_m) range = 58⁰-60⁰ C, primer optimal T_m = 59⁰ C, maximum primer difference = 2⁰ C, probe does not have 5' G, probe T_m must be 10⁰ C greater than primer T_m , amplicon size 75 bp to 100 bp. The probes and primers selected (see below) were synthesized by SyntheGen (Houston, TX, USA). Probes were double purified by HPLC to remove uncoupled dye and evaluated by mass spectroscopy to verify coupling of reporter and quencher dyes to the 5' and 3' ends of the probe, respectively. Their final concentrations were: forward and reverse primers, 900 nM each, and probe, 200nM.

PCR conditions: Normalized RNA from each tissue and each cell line was spotted in each well of a 96 well PCR plate (Perkin Elmer Biosystems). PCR cocktails including two

probes (a probe specific for the target clone and another gene-specific probe multiplexed with the target probe) were set up using 1X TaqMan™ PCR Master Mix for the PE Biosystems 7700, with 5 mM MgCl₂, dNTPs (dA, G, C, U at 1:1:1:2 ratios), 0.25 U/ml AmpliTaq Gold™ (PE Biosystems), and 0.4 U/μl RNase inhibitor, and 0.25 U/μl reverse transcriptase. Reverse transcription was performed at 48° C for 30 minutes followed by amplification/PCR cycles as follows: 95° C 10 min, then 40 cycles of 95° C for 15 seconds, 60° C for 1 minute.

Panel 1

In the results for Panel 1, the following abbreviations are used:

ca. = carcinoma,
* = established from metastasis,
met = metastasis,
s cell var= small cell variant,
non-s = non-sm =non-small,
squam = squamous,
pl. eff = pl effusion = pleural effusion,
glio = glioma,
astro = astrocytoma, and
neuro = neuroblastoma.

Panel 2

The plates for Panel 2 generally include 2 control wells and 94 test samples composed of RNA or cDNA isolated from human tissue procured by surgeons working in close cooperation with the National Cancer Institute's Cooperative Human Tissue Network (CHTN) or the National Disease Research Initiative (NDRI). The tissues are derived from human malignancies and in cases where indicated many malignant tissues have "matched margins" obtained from noncancerous tissue just adjacent to the tumor. These are termed normal adjacent tissues and are denoted "NAT" in the results below. The tumor tissue and the "matched margins" are evaluated by two independent pathologists (the surgical pathologists and again by a pathologists at NDRI or CHTN). This analysis provides a gross histopathological assessment of tumor differentiation grade. Moreover, most samples include the original surgical pathology report that provides information regarding the clinical stage of the patient. These matched margins are taken from the tissue surrounding (*i.e.* immediately proximal) to the zone of surgery (designated "NAT", for normal adjacent tissue). In addition, RNA and cDNA samples were obtained from various human tissues derived from autopsies performed on elderly people or sudden death victims (accidents, etc.). These tissues were ascertained to be free of

disease and were purchased from various commercial sources such as Clontech (Palo Alto, CA), Research Genetics, and Invitrogen.

RNA integrity from all samples is controlled for quality by visual assessment of agarose gel electropherograms using 28S and 18S ribosomal RNA staining intensity ratio as a guide (2:1 to 2.5:1 28s:18s) and the absence of low molecular weight RNAs that would be indicative of degradation products. Samples are controlled against genomic DNA contamination by RTQ PCR reactions run in the absence of reverse transcriptase using probe and primer sets designed to amplify across the span of a single exon.

Panel 4

Panel 4 includes samples on a 96 well plate (2 control wells, 94 test samples) composed of RNA (Panel 4r) or cDNA (Panel 4d) isolated from various human cell lines or tissues related to inflammatory conditions. Total RNA from control normal tissues such as colon and lung (Stratagene, La Jolla, CA) and thymus and kidney (Clontech) were employed. Total RNA from liver tissue from cirrhosis patients and kidney from lupus patients was obtained from BioChain (Biochain Institute, Inc., Hayward, CA). Intestinal tissue for RNA preparation from patients diagnosed as having Crohn's disease and ulcerative colitis was obtained from the National Disease Research Interchange (NDRI) (Philadelphia, PA).

Astrocytes, lung fibroblasts, dermal fibroblasts, coronary artery smooth muscle cells, small airway epithelium, bronchial epithelium, microvascular dermal endothelial cells, microvascular lung endothelial cells, human pulmonary aortic endothelial cells, human umbilical vein endothelial cells were all purchased from Clonetics (Walkersville, MD) and grown in the media supplied for these cell types by Clonetics. These primary cell types were activated with various cytokines or combinations of cytokines for 6 and/or 12-14 hours, as indicated. The following cytokines were used; IL-1 beta at approximately 1-5 ng/ml, TNF alpha at approximately 5-10 ng/ml, IFN gamma at approximately 20-50 ng/ml, IL-4 at approximately 5-10 ng/ml, IL-9 at approximately 5-10 ng/ml, IL-13 at approximately 5-10 ng/ml. Endothelial cells were sometimes starved for various times by culture in the basal media from Clonetics with 0.1% serum.

Mononuclear cells were prepared from blood of employees at CuraGen Corporation, using Ficoll. LAK cells were prepared from these cells by culture in DMEM 5% FCS (Hyclone), 100 μ M non essential amino acids (Gibco/Life Technologies, Rockville, MD), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), and 10 mM Hepes

(Gibco) and Interleukin 2 for 4-6 days. Cells were then either activated with 10-20 ng/ml PMA and 1-2 µg/ml ionomycin, IL-12 at 5-10 ng/ml, IFN gamma at 20-50 ng/ml and IL-18 at 5-10 ng/ml for 6 hours. In some cases, mononuclear cells were cultured for 4-5 days in DMEM 5% FCS (Hyclone), 100 µM non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), and 10 mM Hepes (Gibco) with PHA (phytohemagglutinin) or PWM (pokeweed mitogen) at approximately 5 µg/ml. Samples were taken at 24, 48 and 72 hours for RNA preparation. MLR (mixed lymphocyte reaction) samples were obtained by taking blood from two donors, isolating the mononuclear cells using Ficoll and mixing the isolated mononuclear cells 1:1 at a final concentration of approximately 2×10^6 cells/ml in DMEM 5% FCS (Hyclone), 100 µM non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol (5.5×10^{-5} M) (Gibco), and 10 mM Hepes (Gibco). The MLR was cultured and samples taken at various time points ranging from 1- 7 days for RNA preparation.

Monocytes were isolated from mononuclear cells using CD14 Miltenyi Beads, +ve VS selection columns and a Vario Magnet according to the manufacturer's instructions. Monocytes were differentiated into dendritic cells by culture in DMEM 5% fetal calf serum (FCS) (Hyclone, Logan, UT), 100 µM non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), and 10 mM Hepes (Gibco), 50 ng/ml GM-CSF and 5 ng/ml IL-4 for 5-7 days. Macrophages were prepared by culture of monocytes for 5-7 days in DMEM 5% FCS (Hyclone), 100 µM non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), 10 mM Hepes (Gibco) and 10% AB Human Serum or MCSF at approximately 50 ng/ml. Monocytes, macrophages and dendritic cells were stimulated for 6 and 12-14 hours with lipopolysaccharide (LPS) at 100 ng/ml. Dendritic cells were also stimulated with anti-CD40 monoclonal antibody (Pharmingen) at 10 µg/ml for 6 and 12-14 hours.

CD4 lymphocytes, CD8 lymphocytes and NK cells were also isolated from mononuclear cells using CD4, CD8 and CD56 Miltenyi beads, positive VS selection columns and a Vario Magnet according to the manufacturer's instructions. CD45RA and CD45RO CD4 lymphocytes were isolated by depleting mononuclear cells of CD8, CD56, CD14 and CD19 cells using CD8, CD56, CD14 and CD19 Miltenyi beads and positive selection. Then CD45RO beads were used to isolate the CD45RO CD4 lymphocytes with the remaining cells being CD45RA CD4 lymphocytes. CD45RA CD4, CD45RO CD4 and CD8 lymphocytes were

placed in DMEM 5% FCS (Hyclone), 100 μ M non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), and 10 mM Hepes (Gibco) and plated at 10^6 cells/ml onto Falcon 6 well tissue culture plates that had been coated overnight with 0.5 μ g/ml anti-CD28 (Pharmingen) and 3 μ g/ml anti-CD3 (OKT3, ATCC) in PBS. After 6 and 24 hours, the cells were harvested for RNA preparation. To prepare chronically activated CD8 lymphocytes, we activated the isolated CD8 lymphocytes for 4 days on anti-CD28 and anti-CD3 coated plates and then harvested the cells and expanded them in DMEM 5% FCS (Hyclone), 100 μ M non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), and 10 mM Hepes (Gibco) and IL-2. The expanded CD8 cells were then activated again with plate bound anti-CD3 and anti-CD28 for 4 days and expanded as before. RNA was isolated 6 and 24 hours after the second activation and after 4 days of the second expansion culture. The isolated NK cells were cultured in DMEM 5% FCS (Hyclone), 100 μ M non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), and 10 mM Hepes (Gibco) and IL-2 for 4-6 days before RNA was prepared.

To obtain B cells, tonsils were procured from NDRI. The tonsil was cut up with sterile dissecting scissors and then passed through a sieve. Tonsil cells were then spun down and resuspended at 10^6 cells/ml in DMEM 5% FCS (Hyclone), 100 μ M non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), and 10 mM Hepes (Gibco). To activate the cells, we used PWM at 5 μ g/ml or anti-CD40 (Pharmingen) at approximately 10 μ g/ml and IL-4 at 5-10 ng/ml. Cells were harvested for RNA preparation at 24, 48 and 72 hours.

To prepare the primary and secondary Th1/Th2 and Tr1 cells, six-well Falcon plates were coated overnight with 10 μ g/ml anti-CD28 (Pharmingen) and 2 μ g/ml OKT3 (ATCC), and then washed twice with PBS. Umbilical cord blood CD4 lymphocytes (Poietic Systems, German Town, MD) were cultured at 10^5 - 10^6 cells/ml in DMEM 5% FCS (Hyclone), 100 μ M non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), 10 mM Hepes (Gibco) and IL-2 (4 ng/ml). IL-12 (5 ng/ml) and anti-IL4 (1 μ g/ml) were used to direct to Th1, while IL-4 (5 ng/ml) and anti-IFN gamma (1 μ g/ml) were used to direct to Th2 and IL-10 at 5 ng/ml was used to direct to Tr1. After 4-5 days, the activated Th1, Th2 and Tr1 lymphocytes were washed once in DMEM and expanded for 4-7 days in DMEM

5% FCS (Hyclone), 100 μ M non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), 10 mM Hepes (Gibco) and IL-2 (1 ng/ml). Following this, the activated Th1, Th2 and Tr1 lymphocytes were re-stimulated for 5 days with anti-CD28/OKT3 and cytokines as described above, but with the addition of anti-CD95L (1 μ g/ml) to prevent apoptosis. After 4-5 days, the Th1, Th2 and Tr1 lymphocytes were washed and then expanded again with IL-2 for 4-7 days. Activated Th1 and Th2 lymphocytes were maintained in this way for a maximum of three cycles. RNA was prepared from primary and secondary Th1, Th2 and Tr1 after 6 and 24 hours following the second and third activations with plate bound anti-CD3 and anti-CD28 mAbs and 4 days into the second and third expansion cultures in Interleukin 2.

The following leukocyte cells lines were obtained from the ATCC: Ramos, EOL-1, KU-812. EOL cells were further differentiated by culture in 0.1 mM dbcAMP at 5×10^5 cells/ml for 8 days, changing the media every 3 days and adjusting the cell concentration to 5×10^5 cells/ml. For the culture of these cells, we used DMEM or RPMI (as recommended by the ATCC), with the addition of 5% FCS (Hyclone), 100 μ M non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), 10 mM Hepes (Gibco). RNA was either prepared from resting cells or cells activated with PMA at 10 ng/ml and ionomycin at 1 μ g/ml for 6 and 14 hours. Keratinocyte line CCD106 and an airway epithelial tumor line NCI-H292 were also obtained from the ATCC. Both were cultured in DMEM 5% FCS (Hyclone), 100 μ M non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), and 10 mM Hepes (Gibco). CCD1106 cells were activated for 6 and 14 hours with approximately 5 ng/ml TNF alpha and 1 ng/ml IL-1 beta, while NCI-H292 cells were activated for 6 and 14 hours with the following cytokines: 5 ng/ml IL-4, 5 ng/ml IL-9, 5 ng/ml IL-13 and 25 ng/ml IFN gamma.

For these cell lines and blood cells, RNA was prepared by lysing approximately 10^7 cells/ml using Trizol (Gibco BRL). Briefly, 1/10 volume of bromochloropropane (Molecular Research Corporation) was added to the RNA sample, vortexed and after 10 minutes at room temperature, the tubes were spun at 14,000 rpm in a Sorvall SS34 rotor. The aqueous phase was removed and placed in a 15 ml Falcon Tube. An equal volume of isopropanol was added and left at -20 degrees C overnight. The precipitated RNA was spun down at 9,000 rpm for 15 min in a Sorvall SS34 rotor and washed in 70% ethanol. The pellet was redissolved in 300 μ l of RNase-free water and 35 μ l buffer (Promega) 5 μ l DTT, 7 μ l RNAsin and 8 μ l DNase were

added. The tube was incubated at 37 degrees C for 30 minutes to remove contaminating genomic DNA, extracted once with phenol chloroform and re-precipitated with 1/10 volume of 3 M sodium acetate and 2 volumes of 100% ethanol. The RNA was spun down and placed in RNase free water. RNA was stored at -80 degrees C.

- 5 A summary of the TaqMan protocols used for each NOVX is provided in Table B.

Table B. Summary of TaqMan Protocols	
NOVX	Ag#
1	Ag3075
3a	Ag1247
3b	Ag1247
4a	AG1491/Ag676/ Ag1403 (identical) Ag721 Ag2835 Ag396
4b	Ag 721, Ag1491, Ag1403, Ag2835
4c	Ag721, Ag1491, Ag1403, Ag2835
4d	Ag721, Ag1491, Ag1403, Ag2835
6	Ag274
7	Ag582
8a	Ag850
8b	Ag850
8c	Ag217
9	Ag1249

NOV1

Expression of NOV1 was assessed using the primer-probe set Ag3075, described in Table C. Results of the RTQ-PCR runs are shown in Tables D, E and F.

10

Table C. Probe Name: Ag3075

Primers	Sequences	TM	Length	Start Position
Forward	5'-CAAACCTTCTGAGCGAACTCG-3' (SEQ ID NO: 76)	58.8	20	153
Probe	FAM-5'-ATTGGAGAGGGCAGCTACTCCAAGGT-3' - TAMRA (SEQ ID NO: 77)	69.1	26	193
Reverse	5'-TGTAATCTCTTGGATGTGGCC-3' (SEQ ID NO: 78)	58.6	20	225

Table D. Panel 1.3D

Tissue Name	Relative Expression(%) 1.3dx4tm5354f _ag3075_b2	Tissue Name	Relative Expression(%) 1.3dx4tm5354f _ag3075_b2
Liver adenocarcinoma	1.0	Kidney (fetal)	0.4
Pancreas	0.4	Renal ca. 786-0	0.2
Pancreatic ca. CAPAN 2	1.2	Renal ca. A498	0.7
Adrenal gland	1.4	Renal ca. RXF 393	0.6
Thyroid	1.5	Renal ca. ACHN	0.9
Salivary gland	0.2	Renal ca. UO-31	0.7
Pituitary gland	0.9	Renal ca. TK-10	0.2
Brain (fetal)	1.9	Liver	0.4
Brain (whole)	1.2	Liver (fetal)	1.4
Brain (amygdala)	1.2	Liver ca. (hepatoblast) HepG2	0.3
Brain (cerebellum)	1.0	Lung	0.1
Brain (hippocampus)	1.5	Lung (fetal)	0.0
Brain (substantia nigra)	0.7	Lung ca. (small cell) LX-1	0.0
Brain (thalamus)	2.0	Lung ca. (small cell) NCI-H69	0.2
Cerebral Cortex	0.2	Lung ca. (s.cell var.) SHP-77	1.5
Spinal cord	0.8	Lung ca. (large cell) NCI-H460	1.5
CNS ca. (glio/astro) U87-MG	0.7	Lung ca. (non-sm. cell) A549	1.3
CNS ca. (glio/astro) U-118-MG	3.0	Lung ca. (non-s.cell) NCI-H23	0.3
CNS ca. (astro) SW1783	0.5	Lung ca (non-s.cell) HOP-62	0.4
CNS ca.* (neuro; met) SK-N-AS	1.5	Lung ca. (non-s.cl) NCI-H522	0.6
CNS ca. (astro) SF-539	0.8	Lung ca. (squam.) SW 900	1.2
CNS ca. (astro) SNB-75	1.1	Lung ca. (squam.) NCI-H596	0.4
CNS ca. (glio) SNB-19	1.3	Mammary gland	1.3
CNS ca. (glio) U251	1.5	Breast ca.* (pl. effusion) MCF-7	0.0
CNS ca. (glio) SF-295	0.3	Breast ca.* (pl.ef) MDA-MB-231	1.7
Heart (fetal)	0.3	Breast ca.* (pl. effusion) T47D	0.8
Heart	0.5	Breast ca. BT-549	0.3
Fetal Skeletal	0.0	Breast ca. MDA-N	0.4
Skeletal muscle	0.3	Ovary	0.5
Bone marrow	0.0	Ovarian ca. OVCAR-3	1.0
Thymus	2.4	Ovarian ca. OVCAR-4	0.8
Spleen	1.8	Ovarian ca. OVCAR-5	0.5
Lymph node	2.0	Ovarian ca. OVCAR-8	0.2
Colorectal	0.0	Ovarian ca. IGROV-1	0.1
Stomach	2.7	Ovarian ca.* (ascites) SK-OV-3	0.3

WO 01/90155		PCT/US01/17073	
Small intestine	1.6	Uterus	0.4
Colon ca. SW480	0.5	Placenta	0.4
Colon ca.* (SW480 met)SW620	0.3	Prostate	1.5
Colon ca. HT29	0.4	Prostate ca.* (bone met)PC-3	0.7
Colon ca. HCT-116	0.0	Testis	100.0
Colon ca. CaCo-2	0.4	Melanoma Hs688(A).T	0.4
83219 CC Well to Mod Diff (ODO3866)	0.2	Melanoma* (met) Hs688(B).T	0.2
Colon ca. HCC-2998	0.3	Melanoma UACC-62	1.3
Gastric ca.* (liver met) NCI-N87	3.2	Melanoma M14	1.6
Bladder	0.2	Melanoma LOX IMVI	0.4
Trachea	0.6	Melanoma* (met) SK-MEL-5	0.5
Kidney	0.2	Adipose	0.2

Table E. Panel 2D

Tissue Name	Relative Expression(%) 2dx4tm4819f_ ag3075_b2	Tissue Name	Relative Expression(%) 2dx4tm4819f_ ag3075_b2
Normal Colon GENPAK 061003	11.1	Kidney NAT Clontech 8120608	20.4
83219 CC Well to Mod Diff (ODO3866)	6.6	Kidney Cancer Clontech 8120613	54.3
83220 CC NAT (ODO3866)	9.2	Kidney NAT Clontech 8120614	25.5
83221 CC Gr.2 rectosigmoid (ODO3868)	3.0	Kidney Cancer Clontech 9010320	25.0
83222 CC NAT (ODO3868)	0.8	Kidney NAT Clontech 9010321	16.9
83235 CC Mod Diff (ODO3920)	15.2	Normal Uterus GENPAK 061018	1.1
83236 CC NAT (ODO3920)	12.0	Uterus Cancer GENPAK 064011	15.9
83237 CC Gr.2 ascend colon (ODO3921)	9.2	Normal Thyroid Clontech A+ 6570-1	27.8
83238 CC NAT (ODO3921)	17.3	Thyroid Cancer GENPAK 064010	7.6
83241 CC from Partial Hepatectomy (ODO4309)	15.3	Thyroid Cancer INVITROGEN A302152	12.4
83242 Liver NAT (ODO4309)	13.7	Thyroid NAT INVITROGEN A302153	27.7
87472 Colon mets to lung (OD04451-01)	0.8	Normal Breast GENPAK 061019	12.7
87473 Lung NAT (OD04451-02)	8.4	84877 Breast Cancer (OD04566)	10.7
Normal Prostate Clontech A+ 6546-1	58.6	85975 Breast Cancer (OD04590-01)	86.1

84140 Prostate Cancer (OD04410)	15.8	85976 Breast Cancer Mets (OD04590-03)	100.0
84141 Prostate NAT (OD04410)	17.5	87070 Breast Cancer Metastasis (OD04655-05)	59.8
87073 Prostate Cancer (OD04720-01)	22.9	GENPAK Breast Cancer 064006	6.9
87074 Prostate NAT (OD04720-02)	18.4	Breast Cancer Res. Gen. 1024	12.6
Normal Lung GENPAK 061010	29.5	Breast Cancer Clontech 9100266	22.4
83239 Lung Met to Muscle (ODO4286)	11.5	Breast NAT Clontech 9100265	7.2
83240 Muscle NAT (ODO4286)	1.7	Breast Cancer INVITROGEN A209073	13.6
84136 Lung Malignant Cancer (OD03126)	44.6	Breast NAT INVITROGEN A2090734	12.5
84137 Lung NAT (OD03126)	23.7	Normal Liver GENPAK 061009	7.0
84871 Lung Cancer (OD04404)	13.9	Liver Cancer GENPAK 064003	3.8
84872 Lung NAT (OD04404)	13.0	Liver Cancer Research Genetics RNA 1025	3.6
84875 Lung Cancer (OD04565)	1.1	Liver Cancer Research Genetics RNA 1026	8.1
84876 Lung NAT (OD04565)	7.2	Paired Liver Cancer Tissue Research Genetics RNA 6004- T	7.2
85950 Lung Cancer (OD04237- 01)	60.5	Paired Liver Tissue Research Genetics RNA 6004-N	11.5
85970 Lung NAT (OD04237- 02)	7.1	Paired Liver Cancer Tissue Research Genetics RNA 6005- T	11.4
83255 Ocular Mel Met to Liver (ODO4310)	15.0	Paired Liver Tissue Research Genetics RNA 6005-N	1.8
83256 Liver NAT (ODO4310)	6.8	Normal Bladder GENPAK 061001	17.1
84139 Melanoma Mets to Lung (OD04321)	6.9	Bladder Cancer Research Genetics RNA 1023	5.7
84138 Lung NAT (OD04321)	15.3	Bladder Cancer INVITROGEN A302173	11.8
Normal Kidney GENPAK 061008	34.7	87071 Bladder Cancer (OD04718-01)	7.8
83786 Kidney Ca, Nuclear grade 2 (OD04338)	15.8	87072 Bladder Normal Adjacent (OD04718-03)	3.8
83787 Kidney NAT (OD04338)	27.7	Normal Ovary Res. Gen.	3.7
83788 Kidney Ca Nuclear grade 1/2 (OD04339)	17.4	Ovarian Cancer GENPAK 064008	24.3
83789 Kidney NAT (OD04339)	29.3	87492 Ovary Cancer (OD04768-07)	38.6
83790 Kidney Ca, Clear cell	3.2	87493 Ovary NAT (OD04768-	6.3

type (OD04340)		08)	
83791 Kidney NAT (OD04340)	22.4	Normal Stomach GENPAK 061017	7.9
83792 Kidney Ca, Nuclear grade 3 (OD04348)	13.2	Gastric Cancer Clontech 9060358	1.8
83793 Kidney NAT (OD04348)	17.2	NAT Stomach Clontech 9060359	4.7
87474 Kidney Cancer (OD04622-01)	18.5	Gastric Cancer Clontech 9060395	14.0
87475 Kidney NAT (OD04622- 03)	7.5	NAT Stomach Clontech 9060394	16.4
85973 Kidney Cancer (OD04450-01)	47.3	Gastric Cancer Clontech 9060397	15.0
85974 Kidney NAT (OD04450- 03)	24.4	NAT Stomach Clontech 9060396	6.5
Kidney Cancer Clontech 8120607	21.5	Gastric Cancer GENPAK 064005	15.0

Table F. Panel 4D

Tissue Name	Relative Expression(%) 4dtm4708f_ag 3075	Tissue Name	Relative Expression(%) 4dtm4708f_ag 3075
93768_Secondary Th1_anti- CD28/anti-CD3	33.9	93100_HUVEC (Endothelial)_IL-1b	0.0
93769_Secondary Th2_anti- CD28/anti-CD3	43.5	93779_HUVEC (Endothelial)_IFN gamma	11.2
93770_Secondary Tr1_anti- CD28/anti-CD3	35.1	93102_HUVEC (Endothelial)_TNF alpha + IFN gamma	7.2
93573_Secondary Th1_resting day 4-6 in IL-2	20.0	93101_HUVEC (Endothelial)_TNF alpha + IL4	6.7
93572_Secondary Th2_resting day 4-6 in IL-2	19.6	93781_HUVEC (Endothelial)_IL-11	8.5
93571_Secondary Tr1_resting day 4-6 in IL-2	21.2	93583_Lung Microvascular Endothelial Cells_none	3.2
93568_primary Th1_anti- CD28/anti-CD3	22.5	93584_Lung Microvascular Endothelial Cells_TNFa (4 ng/ml) and IL1b (1 ng/ml)	18.6
93569_primary Th2_anti- CD28/anti-CD3	35.4	92662_Microvascular Dermal endothelium_none	4.2
93570_primary Tr1_anti- CD28/anti-CD3	54.0	92663_Microvascular Dermal endothelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	3.7
93565_primary Th1_resting dy 4-6 in IL-2	73.7	93773_Bronchial epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml) **	0.0

93566_primary Th2_resting dy 4-6 in IL-2	41.5	93347_Small Airway Epithelium_none	9.9
93567_primary Tr1_resting dy 4-6 in IL-2	42.3	93348_Small Airway Epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	21.3
93351_CD45RA CD4 lymphocyte_anti-CD28/anti- CD3	0.0	92668_Coronary Artery SMC_resting	8.8
93352_CD45RO CD4 lymphocyte_anti-CD28/anti- CD3	36.6	92669_Coronary Artery SMC_TNFa (4 ng/ml) and IL1b (1 ng/ml)	8.1
93251_CD8 Lymphocytes_anti- CD28/anti-CD3	27.2	93107_astrocytes_resting	9.4
93353_chronic CD8 Lymphocytes 2ry_resting dy 4- 6 in IL-2	47.0	93108_astrocytes_TNFa (4 ng/ml) and IL1b (1 ng/ml)	3.8
93574_chronic CD8 Lymphocytes 2ry_activated CD3/CD28	18.0	92666_KU-812 (Basophil)_resting	67.8
93354_CD4_none	23.8	92667_KU-812 (Basophil)_PMA/ionoycin	80.7
93252_Secondary Th1/Th2/Tr1_anti-CD95 CH11	23.8	93579_CCD1106 (Keratinocytes)_none	31.2
93103_LAK cells_resting	17.9	93580_CCD1106 (Keratinocytes)_TNFa and IFNg **	5.8
93788_LAK cells_IL-2	30.1	93791_Liver Cirrhosis	7.1
93787_LAK cells_IL-2+IL-12	54.0	93792_Lupus Kidney	0.8
93789_LAK cells_IL-2+IFN gamma	51.8	93577_NCI-H292	100.0
93790_LAK cells_IL-2+ IL-18	45.7	93358_NCI-H292_IL-4	57.4
93104_LAK cells_PMA/ionomycin and IL- 18	14.0	93360_NCI-H292_IL-9	77.4
93578_NK Cells IL-2_resting	28.1	93359_NCI-H292_IL-13	69.3
93109_Mixed Lymphocyte Reaction_Two Way MLR	24.8	93357_NCI-H292_IFN gamma	71.7
93110_Mixed Lymphocyte Reaction_Two Way MLR	13.1	93777_HPAEC_-	6.7
93111_Mixed Lymphocyte Reaction_Two Way MLR	22.8	93778_HPAEC_IL-1 beta/TNA alpha	9.1
93112_Mononuclear Cells (PBMCs)_resting	6.0	93254_Normal Human Lung Fibroblast_none	22.4
93113_Mononuclear Cells (PBMCs)_PWM	31.6	93253_Normal Human Lung Fibroblast_TNFa (4 ng/ml) and IL-1b (1 ng/ml)	10.7
93114_Mononuclear Cells (PBMCs)_PHA-L	13.4	93257_Normal Human Lung Fibroblast_IL-4	32.1
93249_Ramos (B cell)_none	33.9	93256_Normal Human Lung	20.9

		Fibroblast_IL-9	
93250_Ramos (B cell)_ionomycin	37.6	93255_Normal Human Lung Fibroblast_IL-13	33.4
93349_B lymphocytes_PWM	64.6	93258_Normal Human Lung Fibroblast_IFN gamma	35.8
93350_B lymphocytes_CD40L and IL-4	42.0	93106_Dermal Fibroblasts CCD1070_resting	12.9
92665_EOL-1 (Eosinophil)_dbcAMP differentiated	92.7	93361_Dermal Fibroblasts CCD1070_TNF alpha 4 ng/ml	54.0
93248_EOL-1 (Eosinophil)_dbcAMP/PMAionomycin	42.6	93105_Dermal Fibroblasts CCD1070_IL-1 beta 1 ng/ml	5.8
93356_Dendritic Cells_none	18.7	93772_dermal fibroblast_IFN gamma	14.9
93355_Dendritic Cells_LPS 100 ng/ml	23.5	93771_dermal fibroblast_IL-4	18.7
93775_Dendritic Cells_anti-CD40	18.0	93259_IBD Colitis 1**	3.5
93774_Monocytes_resting	3.1	93260_IBD Colitis 2	0.0
93776_Monocytes_LPS 50 ng/ml	3.6	93261_IBD Crohns	3.5
93581_Macrophages_resting	21.8	735010_Colon_normal	44.4
93582_Macrophages_LPS 100 ng/ml	8.3	735019_Lung_none	29.3
93098_HUVEC (Endothelial)_none	6.8	64028-1_Thymus_none	48.3
93099_HUVEC (Endothelial)_starved	4.0	64030-1_Kidney_none	37.9

Panel 1.3D Summary: NOV1 is highly expressed in the testis, with expression levels being at least an order of magnitude lower in other tissues. Therefore this gene may be a marker for the testis and may be important in the regulation or dysregulation of spermatogenesis and fertility. Among other normal tissues, expression is detected at lower levels in fetal and adult brain; thyroid, adrenal and pituitary glands, thymus, spleen, lymph node, small intestine, fetal liver, mammary gland, prostate and spinal cord. In disease conditions, the highest expression is seen in a sample of gastric cancer, followed by CNS cancers, melanomas, lung, breast, pancreatic, liver and ovarian cancers. Therapeutics designed to this molecule may be effective in the treatment of infertility or cancer.

Panel 2D Summary: This gene is expressed across a wide number of samples in panel 2D. Particularly it appears to be overexpressed in breast cancers relative to normal tissues as

well as ovarian, kidney and lung cancers. Thus, inhibition of NOV1 function might be useful in the therapy of these or potentially other cancer types.

Panel 4D Summary: The NOV1 transcript is expressed in many tissues regardless of treatment with the exception of colitis/inflammatory bowel disease (IBD) samples.

- 5 Therapeutics designed to replace the protein encoded for by this transcript may reduce or eliminate inflammation due to inflammatory bowel diseases.

NOV3A

Expression of NOV3a was assessed using the primer-probe set Ag1247, described in Table G. Results of the RTQ-PCR runs are shown in Table H.

Table G. Probe Name: Ag1247

Primers	Sequences	TM	Length	Start Position
Forward	5'-GAATAGCTCCTGCTTGGATTTT-3' (SEQ ID NO: 79)	58.9	22	1413
Probe	FAM-5'-CTCACCTCTGCCTTCAGTCACTGGG-3' - TAMRA (SEQ ID NO: 80)	69.6	25	1455
Reverse	5'-CTGCCTGTCTTACCATTGATGT-3' (SEQ ID NO: 81)	59.1	22	1486

Table H. Panel 4D

Tissue Name	Relative Expression(%) 4Dtm2106f_ag 1247	Tissue Name	Relative Expression(%) 4Dtm2106f_ag 1247
93768_Secondary Th1_anti-CD28/anti-CD3	0.0	93100_HUVEC (Endothelial)_IL-1b	0.0
93769_Secondary Th2_anti-CD28/anti-CD3	0.0	93779_HUVEC (Endothelial)_IFN gamma	0.0
93770_Secondary Tr1_anti-CD28/anti-CD3	0.0	93102_HUVEC (Endothelial)_TNF alpha + IFN gamma	0.0
93573_Secondary Th1_resting day 4-6 in IL-2	0.0	93101_HUVEC (Endothelial)_TNF alpha + IL4	0.0
93572_Secondary Th2_resting day 4-6 in IL-2	0.0	93781_HUVEC (Endothelial)_IL-11	0.0
93571_Secondary Tr1_resting	0.0	93583_Lung Microvascular	0.0

day 4-6 in IL-2		Endothelial Cells_none	
93568_primary Th1_anti- CD28/anti-CD3	0.0	93584_Lung Microvascular Endothelial Cells_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0.0
93569_primary Th2_anti- CD28/anti-CD3	0.0	92662_Microvascular Dermal endothelium_none	0.0
93570_primary Tr1_anti- CD28/anti-CD3	5.3	92663_Microvascular Dermal endothelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0.0
93565_primary Th1_resting dy 4-6 in IL-2	0.0	93773_Bronchial epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml) **	0.0
93566_primary Th2_resting dy 4-6 in IL-2	0.0	93347_Small Airway Epithelium_none	0.0
93567_primary Tr1_resting dy 4-6 in IL-2	0.0	93348_Small Airway Epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0.0
93351_CD45RA CD4 lymphocyte_anti-CD28/anti- CD3	0.0	92668_Coronary Artery SMC_resting	0.0
93352_CD45RO CD4 lymphocyte_anti-CD28/anti- CD3	7.6	92669_Coronary Artery SMC_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0.0
93251_CD8 Lymphocytes_anti- CD28/anti-CD3	0.0	93107_astrocytes_resting	8.0
93353_chronic CD8 Lymphocytes 2ry_resting dy 4- 6 in IL-2	0.0	93108_astrocytes_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0.0
93574_chronic CD8 Lymphocytes 2ry_activated CD3/CD28	0.0	92666_KU-812 (Basophil)_resting	0.0
93354_CD4_none	0.0	92667_KU-812 (Basophil)_PMA/ionomycin	0.0
93252_Secondary Th1/Th2/Tr1_anti-CD95 CH11	0.0	93579_CCD1106 (Keratinocytes)_none	0.0
93103_LAK cells_resting	0.0	93580_CCD1106 (Keratinocytes)_TNFa and IFNg **	0.0
93788_LAK cells_IL-2	18.6	93791_Liver Cirrhosis	16.8
93787_LAK cells_IL-2+IL-12	0.0	93792_Lupus Kidney	0.0
93789_LAK cells_IL-2+IFN gamma	0.0	93577_NCI-H292	0.0
93790_LAK cells_IL-2+ IL-18	8.6	93358_NCI-H292_IL-4	0.0
93104_LAK cells_PMA/ionomycin and IL- 18	0.0	93360_NCI-H292_IL-9	0.0
93578_NK Cells IL-2_resting	0.0	93359_NCI-H292_IL-13	0.0
93109_Mixed Lymphocyte Reaction_Two Way MLR	0.0	93357_NCI-H292_IFN gamma	0.0

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93110_Mixed Lymphocyte Reaction_Two Way MLR	0.0	93777_HPAEC_-	0.0
93111_Mixed Lymphocyte Reaction_Two Way MLR	0.0	93778_HPAEC_IL-1 beta/TNA alpha	0.0
93112_Mononuclear Cells (PBMcs)_resting	0.0	93254_Normal Human Lung Fibroblast_none	0.0
93113_Mononuclear Cells (PBMcs)_PWM	0.0	93253_Normal Human Lung Fibroblast_TNFa (4 ng/ml) and IL-1b (1 ng/ml)	0.0
93114_Mononuclear Cells (PBMcs)_PHA-L	0.0	93257_Normal Human Lung Fibroblast_IL-4	0.0
93249_Ramos (B cell)_none	0.0	93256_Normal Human Lung Fibroblast_IL-9	0.0
93250_Ramos (B cell)_ionomycin	0.0	93255_Normal Human Lung Fibroblast_IL-13	0.0
93349_B lymphocytes_PWM	7.3	93258_Normal Human Lung Fibroblast_IFN gamma	0.0
93350_B lymphocytes_CD40L and IL-4	0.0	93106_Dermal Fibroblasts CCD1070_resting	0.0
92665_EOL-1 (Eosinophil)_dbcAMP differentiated	0.0	93361_Dermal Fibroblasts CCD1070_TNF alpha 4 ng/ml	0.0
93248_EOL-1 (Eosinophil)_dbcAMP/PMAionomycin	0.0	93105_Dermal Fibroblasts CCD1070_IL-1 beta 1 ng/ml	0.0
93356_Dendritic Cells_none	0.0	93772_dermal fibroblast_IFN gamma	0.0
93355_Dendritic Cells_LPS 100 ng/ml	0.0	93771_dermal fibroblast_IL-4	0.0
93775_Dendritic Cells_anti-CD40	0.0	93259_IBD Colitis 1**	100.0
93774_Monocytes_resting	0.0	93260_IBD Colitis 2	0.0
93776_Monocytes_LPS 50 ng/ml	0.0	93261_IBD Crohns	0.0
93581_Macrophages_resting	0.0	735010_Colon_normal	0.0
93582_Macrophages_LPS 100 ng/ml	0.0	735019_Lung_none	11.8
93098_HUVEC (Endothelial)_none	0.0	64028-1_Thymus_none	0.0
93099_HUVEC (Endothelial)_starved	0.0	64030-1_Kidney_none	0.0

Panel 4D Summary: High expression of the NOV3a transcript is seen in colitis 1. The protein encoded for by this antigen may be important in the inflammatory process. Antagonistic antibodies or small molecule therapeutics may reduce or inhibit inflammation in the bowel due to IBD.

NOV4a

Expression of NOV4a was assessed using the primer-probe sets Ag1491, Ag676 and Ag1403 (identical sequences), Ag721 and Ag2835, described in Tables I, J and K. Results of the RTQ-PCR runs are shown in Tables L, M, N and O.

5 Table I. Probe Name: Ag1491/Ag676/Ag1403

Primers	Sequences	TM	Length	Start Position
Forward	5'-TAATGGAGAAGGCAGCAGAAG-3' (SEQ ID NO: 82)	59.6	21	1604
Probe	TET-5'-TCTATACCCGGCTCAAGTCGCGG-3' -TAMRA (SEQ ID NO: 83)	70.2	23	1625
Reverse	5'-CCCAGCCTTGTTCACTTTCT-3' (SEQ ID NO: 84)	59.3	20	1676

Table J. Probe Name: Ag721

Primers	Sequences	TM	Length	Start Position
Forward	5'-ACCCAACAAGTACCCCATCTT-3' (SEQ ID NO: 104)	59.6	21	108
Probe	FAM-5'-TTTCTTTGGCACACACGAAACGG-3' -TAMRA (SEQ ID NO: 105)	68.2	23	129
Reverse	5'-TACATTTGTCGTAGGGGAACAG-3' (SEQ ID NO: 106)	59	22	172

10 Table K. Probe Name: Ag2835

Primers	Sequences	TM	Length	Start Position
Forward	5'-GACCTTTAGGGCAAACCTTGATC-3' (SEQ ID NO: 107)	59.1	22	757
Probe	TET-5'-ACTGTGCAGCTTCTGCAGCTTCTCCT-3' -TAMRA (SEQ ID NO: 108)	69.8	26	781
Reverse	5'-TGGACAGGAAGGTAGAGAAGAA-3' (SEQ ID NO: 109)	58.1	22	824

Table L: Panel 1.2

Tissue Name	Relative Expression(%)	Relative Expression(%)	Relative Expression(%)
	1.2tm1686f_ag1403*	1.2tm895f_ag721	1.2tm2100t_ag1491
Endothelial cells	17.0	27.5	27.7
Endothelial cells (treated)	7.9	7.5	9.7
Pancreas	1.4	33.0	5.7
Pancreatic ca. CAPAN 2	8.6	2.9	3.4
Adrenal Gland (new lot*)	25.7	15.5	23.2
Thyroid	1.2	24.1	2.2
Salivary gland	18.0	14.2	18.2
Pituitary gland	0.8	42.6	0.8
Brain (fetal)	2.6	12.4	0.9
Brain (whole)	8.9	27.7	2.1
Brain (amygdala)	10.6	8.8	6.5
Brain (cerebellum)	4.3	9.4	4.2
Brain (hippocampus)	27.5	16.6	20.6
Brain (thalamus)	16.0	9.3	11.3
Cerebral Cortex	38.4	23.0	42.6
Spinal cord	1.6	9.4	1.4
CNS ca. (glio/astro) U87-MG	17.1	14.9	20.4
CNS ca. (glio/astro) U-118-MG	16.7	12.9	19.8
CNS ca. (astro) SW1783	8.4	5.8	7.5
CNS ca.* (neuro; met) SK-N-AS	24.1	38.7	18.3
CNS ca. (astro) SF-539	8.7	9.8	6.8
CNS ca. (astro) SNB-75	7.0	6.2	5.6
CNS ca. (glio) SNB-19	12.5	9.9	16.0
CNS ca. (glio) U251	6.9	5.7	6.4
CNS ca. (glio) SF-295	32.5	13.2	17.7
Heart	63.3	18.8	62.8
Skeletal Muscle (new lot*)	95.3	100.0	100.0
Bone marrow	6.7	6.0	4.9
Thymus	2.0	7.5	1.7
Spleen	6.2	6.7	5.1
Lymph node	1.2	12.2	0.8
Colorectal	1.0	0.8	1.8
Stomach	3.7	14.5	5.4

Small intestine	21.0	19.1	22.8
Colon ca. SW480	12.0	5.7	14.8
Colon ca.* (SW480 met)SW620	15.6	15.7	17.4
Colon ca. HT29	11.1	8.4	12.0
Colon ca. HCT-116	29.9	13.5	28.1
Colon ca. CaCo-2	15.8	12.2	12.2
83219 CC Well to Mod Diff (ODO3866)	1.2	0.7	1.3
Colon ca. HCC-2998	20.9	8.2	17.6
Gastric ca.* (liver met) NCI-N87	5.6	7.5	6.5
Bladder	17.2	15.5	18.0
Trachea	1.1	7.7	0.5
Kidney	55.1	10.2	47.6
Kidney (fetal)	12.5	22.4	11.9
Renal ca. 786-0	13.9	8.7	17.4
Renal ca. A498	12.9	11.0	14.2
Renal ca. RXF 393	4.3	2.7	5.6
Renal ca. ACHN	20.2	12.8	19.3
Renal ca. UO-31	12.0	4.8	17.9
Renal ca. TK-10	20.6	13.2	19.3
Liver	14.4	8.7	11.2
Liver (fetal)	10.7	8.5	7.8
Liver ca. (hepatoblast) HepG2	17.2	4.5	17.9
Lung	1.0	6.5	0.8
Lung (fetal)	2.8	17.1	2.2
Lung ca. (small cell) LX-1	18.4	10.4	15.8
Lung ca. (small cell) NCI-H69	22.8	11.3	20.9
Lung ca. (s.cell var.) SHP-77	6.7	6.2	5.8
Lung ca. (large cell)NCI-H460	9.6	7.5	12.0
Lung ca. (non-sm. cell) A549	7.0	6.2	7.2
Lung ca. (non-s.cell) NCI-H23	31.0	11.3	19.5
Lung ca (non-s.cell) HOP-62	35.8	16.5	23.7
Lung ca. (non-s.cl) NCI-H522	100.0	53.2	85.9
Lung ca. (squam.) SW 900	17.7	12.5	24.7
Lung ca. (squam.) NCI-H596	33.7	16.4	37.1
Mammary gland	7.3	19.3	3.5
Breast ca.* (pl. effusion) MCF-7	8.4	7.3	8.6

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Breast ca.* (pl.ef) MDA-MB-231	7.6	8.7	6.3
Breast ca.* (pl. effusion) T47D	9.5	10.7	12.0
Breast ca. BT-549	7.9	10.1	6.8
Breast ca. MDA-N	31.9	15.4	18.8
Ovary	21.5	18.4	21.9
Ovarian ca. OVCAR-3	17.0	21.2	20.9
Ovarian ca. OVCAR-4	17.2	8.7	15.4
Ovarian ca. OVCAR-5	33.7	22.4	35.6
Ovarian ca. OVCAR-8	17.6	9.8	21.8
Ovarian ca. IGROV-1	21.2	15.4	24.5
Ovarian ca.* (ascites) SK-OV-3	45.7	29.9	48.6
Uterus	8.8	14.6	6.6
Placenta	1.3	15.5	1.5
Prostate	29.3	18.8	25.0
Prostate ca.* (bone met)PC-3	51.8	35.1	40.3
Testis	4.7	65.5	10.6
Melanoma Hs688(A).T	7.7	5.4	5.8
Melanoma* (met) Hs688(B).T	5.6	4.9	3.3
Melanoma UACC-62	20.2	14.6	18.0
Melanoma M14	10.2	4.9	11.0
Melanoma LOX IMVI	14.4	8.6	9.2
Melanoma* (met) SK-MEL-5	10.7	8.1	8.8
Adipose	10.4	0.7	12.4

Table M. Panel 1.3D

Tissue Name	Relative	Relative
	Expression(%) 1.3Dtm3819t_ag	Expression(%) 1.3dtm4286f_ag
	2835	721
Liver adenocarcinoma	17.0	13.7
Pancreas	7.0	4.5
Pancreatic ca. CAPAN 2	3.5	5.0
Adrenal gland	6.8	5.8
Thyroid	14.9	11.6
Salivary gland	6.4	1.5
Pituitary gland	18.2	11.7
Brain (fetal)	9.3	8.5

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Brain (whole)	19.5	13.0
Brain (amygdala)	19.8	11.6
Brain (cerebellum)	10.4	6.7
Brain (hippocampus)	100.0	62.4
Brain (substantia nigra)	5.7	2.9
Brain (thalamus)	15.1	11.1
Cerebral Cortex	58.6	32.3
Spinal cord	7.8	3.8
CNS ca. (glio/astro) U87-MG	21.8	15.9
CNS ca. (glio/astro) U-118-MG	69.3	74.7
CNS ca. (astro) SW1783	16.3	14.8
CNS ca.* (neuro; met) SK-N-AS	96.6	84.1
CNS ca. (astro) SF-539	15.4	15.5
CNS ca. (astro) SNB-75	19.8	14.8
CNS ca. (glio) SNB-19	8.5	9.7
CNS ca. (glio) U251	7.6	11.2
CNS ca. (glio) SF-295	17.1	23.0
Heart (fetal)	16.2	21.8
Heart	3.7	2.9
Fetal Skeletal	85.9	100.0
Skeletal muscle	11.6	6.2
Bone marrow	9.0	5.3
Thymus	12.0	8.9
Spleen	15.4	10.5
Lymph node	5.4	4.4
Colorectal	8.2	6.0
Stomach	12.3	9.3
Small intestine	20.3	9.1
Colon ca. SW480	21.6	23.7
Colon ca.* (SW480 met)SW620	10.0	14.4
Colon ca. HT29	12.3	11.0
Colon ca. HCT-116	17.8	16.8
Colon ca. CaCo-2	17.8	15.9
83219 CC Well to Mod Diff (ODO3866)	9.9	6.9
Colon ca. HCC-2998	20.0	16.7
Gastric ca.* (liver met) NCI-N87	12.2	9.3
Bladder	4.8	2.8
Trachea	24.5	17.7
Kidney	5.3	3.5
Kidney (fetal)	12.2	8.5
Renal ca. 786-0	17.0	17.8
Renal ca. A498	36.9	32.1

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Renal ca. RXF 393	3.9	3.6
Renal ca. ACHN	7.8	10.0
Renal ca. UO-31	15.5	23.0
Renal ca. TK-10	7.4	8.4
Liver	6.1	1.5
Liver (fetal)	14.5	6.5
Liver ca. (hepatoblast) HepG2	10.0	12.0
Lung	19.6	8.8
Lung (fetal)	20.3	10.2
Lung ca. (small cell) LX-1	5.3	5.6
Lung ca. (small cell) NCI-H69	25.3	27.2
Lung ca. (s.cell var.) SHP-77	23.0	29.1
Lung ca. (large cell) NCI-H460	3.5	1.9
Lung ca. (non-sm. cell) A549	5.4	3.8
Lung ca. (non-s.cell) NCI-H23	18.0	18.3
Lung ca (non-s.cell) HOP-62	9.2	13.2
Lung ca. (non-s.cl) NCI-H522	14.1	15.7
Lung ca. (squam.) SW 900	6.7	4.5
Lung ca. (squam.) NCI-H596	13.4	9.1
Mammary gland	19.2	14.8
Breast ca.* (pl. effusion) MCF-7	5.9	5.3
Breast ca.* (pl.ef) MDA-MB-231	61.6	50.7
Breast ca.* (pl. effusion) T47D	3.9	3.6
Breast ca. BT-549	48.3	39.8
Breast ca. MDA-N	11.7	13.0
Ovary	42.9	43.8
Ovarian ca. OVCAR-3	11.7	10.3
Ovarian ca. OVCAR-4	2.5	4.4
Ovarian ca. OVCAR-5	13.3	21.9
Ovarian ca. OVCAR-8	16.4	16.3
Ovarian ca. IGROV-1	4.7	4.8
Ovarian ca.* (ascites) SK-OV-3	21.6	20.3
Uterus	15.6	9.7
Placenta	12.9	7.8
Prostate	9.3	9.3
Prostate ca.* (bone met) PC-3	17.6	15.6
Testis	56.3	59.0
Melanoma Hs688(A).T	9.4	5.7
Melanoma* (met) Hs688(B).T	4.6	3.6
Melanoma UACC-62	2.9	2.9
Melanoma M14	3.8	3.2
Melanoma LOX IMVI	18.0	20.9

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Melanoma* (met) SK-MEL-5	6.3	5.9
Adipose	5.7	3.3

Table N. Panels 2D and 3D

Panel 2D Tissue Name	Relative Expression(%) 2dtm4287f_ag 721	Panel 3D Tissue Name	Relative Expression(%) 3dtm3957f_ag 721
Normal Colon GENPAK 061003	55.5	94905_Daoy_Medulloblastoma/ Cerebellum_sscDNA	9.3
83219 CC Well to Mod Diff (ODO3866)	11.1	94906_TE671_Medulloblastom /Cerebellum_sscDNA	9.9
83220 CC NAT (ODO3866)	9.4	94907_D283 Med_Medulloblastoma/Cerebel lum_sscDNA	35.1
83221 CC Gr.2 rectosigmoid (ODO3868)	27.9	94908_PFSK-1_Primitive Neuroectodermal/Cerebellum_s scDNA	30.1
83222 CC NAT (ODO3868)	5.5	94909_XF-498_CNS_sscDNA	16.2
83235 CC Mod Diff (ODO3920)	33.4	94910_SNB- 78_CNS/glioma_sscDNA	29.9
83236 CC NAT (ODO3920)	17.8	94911_SF- 268_CNS/glioblastoma_sscDN A	21.3
83237 CC Gr.2 ascend colon (ODO3921)	32.5	94912_T98G_Glioblastoma_ssc DNA	21.5
83238 CC NAT (ODO3921)	11.0	96776_SK-N- SH_Neuroblastoma (metastasis)_sscDNA	31.9
83241 CC from Partial Hepatectomy (ODO4309)	26.1	94913_SF- 295_CNS/glioblastoma_sscDN A	19.5
83242 Liver NAT (ODO4309)	19.2	94914_Cerebellum_sscDNA	15.6
87472 Colon mets to lung (OD04451-01)	17.9	96777_Cerebellum_sscDNA	16.2
87473 Lung NAT (OD04451- 02)	14.0	94916_NCI- H292_Mucoepidermoid lung carcinoma_sscDNA	19.2
Normal Prostate Clontech A+ 6546-1	26.4	94917_DMS-114_Small cell lung cancer_sscDNA	18.9
84140 Prostate Cancer (OD04410)	36.9	94918_DMS-79_Small cell lung cancer/neuroendocrine_sscDN A	100.0

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84141 Prostate NAT (OD04410)	37.9	94919_NCI-H146_Small cell lung cancer/neuroendocrine_sscDN A	18.9
87073 Prostate Cancer (OD04720-01)	40.3	94920_NCI-H526_Small cell lung cancer/neuroendocrine_sscDN A	25.0
87074 Prostate NAT (OD04720-02)	46.3	94921_NCI-N417_Small cell lung cancer/neuroendocrine_sscDN A	15.3
Normal Lung GENPAK 061010	35.1	94923_NCI-H82_Small cell lung cancer/neuroendocrine_sscDN A	17.7
83239 Lung Met to Muscle (ODO4286)	19.3	94924_NCI-H157_Squamous cell lung cancer (metastasis)_sscDNA	18.0
83240 Muscle NAT (ODO4286)	35.6	94925_NCI-H1155_Large cell lung cancer/neuroendocrine_sscDN A	41.8
84136 Lung Malignant Cancer (OD03126)	38.7	94926_NCI-H1299_Large cell lung cancer/neuroendocrine_sscDN A	44.1
84137 Lung NAT (OD03126)	38.4	94927_NCI-H727_Lung carcinoid_sscDNA	18.2
84871 Lung Cancer (OD04404)	37.6	94928_NCI-UMC-11_Lung carcinoid_sscDNA	29.9
84872 Lung NAT (OD04404)	26.2	94929_LX-1_Small cell lung cancer_sscDNA	12.3
84875 Lung Cancer (OD04565)	15.2	94930_Colo-205_Colon cancer_sscDNA	5.1
84876 Lung NAT (OD04565)	13.8	94931_KM12_Colon cancer_sscDNA	17.6
85950 Lung Cancer (OD04237- 01)	100.0	94932_KM20L2_Colon cancer_sscDNA	8.8
85970 Lung NAT (OD04237- 02)	26.2	94933_NCI-H716_Colon cancer_sscDNA	10.2
83255 Ocular Mel Met to Liver (ODO4310)	23.5	94935_SW-48_Colon adenocarcinoma_sscDNA	6.5
83256 Liver NAT (ODO4310)	10.4	94936_SW1116_Colon adenocarcinoma_sscDNA	10.7
84139 Melanoma Mets to Lung (OD04321)	37.4	94937_LS 174T_Colon adenocarcinoma_sscDNA	7.7
84138 Lung NAT (OD04321)	23.2	94938_SW-948_Colon adenocarcinoma_sscDNA	1.1
Normal Kidney GENPAK	50.3	94939_SW-480_Colon	13.2

061008		adenocarcinoma_sscDNA	
83786 Kidney Ca, Nuclear grade 2 (OD04338)	51.0	94940_NCI-SNU-5_Gastric carcinoma_sscDNA	18.9
83787 Kidney NAT (OD04338)	46.0	94941_KATO III_Gastric carcinoma_sscDNA	16.8
83788 Kidney Ca Nuclear grade 1/2 (OD04339)	72.2	94943_NCI-SNU-16_Gastric carcinoma_sscDNA	24.7
83789 Kidney NAT (OD04339)	51.4	94944_NCI-SNU-1_Gastric carcinoma_sscDNA	12.4
83790 Kidney Ca, Clear cell type (OD04340)	42.0	94946_RF-1_Gastric adenocarcinoma_sscDNA	10.6
83791 Kidney NAT (OD04340)	36.3	94947_RF-48_Gastric adenocarcinoma_sscDNA	13.1
83792 Kidney Ca, Nuclear grade 3 (OD04348)	23.0	96778_MKN-45_Gastric carcinoma_sscDNA	18.4
83793 Kidney NAT (OD04348)	29.9	94949_NCI-N87_Gastric carcinoma_sscDNA	5.3
87474 Kidney Cancer (OD04622-01)	24.5	94951_OVCAR-5_Ovarian carcinoma_sscDNA	5.8
87475 Kidney NAT (OD04622-03)	7.6	94952_RL95-2_Uterine carcinoma_sscDNA	7.3
85973 Kidney Cancer (OD04450-01)	32.1	94953_HelaS3_Cervical adenocarcinoma_sscDNA	12.3
85974 Kidney NAT (OD04450-03)	35.1	94954_Ca Ski_Cervical epidermoid carcinoma (metastasis)_sscDNA	26.1
Kidney Cancer Clontech 8120607	28.9	94955_ES-2_Ovarian clear cell carcinoma_sscDNA	19.6
Kidney NAT Clontech 8120608	25.5	94957_Ramos/6h stim_"; Stimulated with PMA/ionomycin 6h_sscDNA	9.3
Kidney Cancer Clontech 8120613	37.9	94958_Ramos/14h stim_"; Stimulated with PMA/ionomycin 14h_sscDNA	9.3
Kidney NAT Clontech 8120614	34.6	94962_MEG-01_Chronic myelogenous leukemia (megokaryoblast)_sscDNA	10.1
Kidney Cancer Clontech 9010320	55.1	94963_Raji_Burkitt's lymphoma_sscDNA	15.1
Kidney NAT Clontech 9010321	49.0	94964_Daudi_Burkitt's lymphoma_sscDNA	16.3
Normal Uterus GENPAK 061018	10.3	94965_U266_B-cell plasmacytoma/myeloma_sscDNA	17.3
Uterus Cancer GENPAK 064011	52.1	94968_CA46_Burkitt's lymphoma_sscDNA	7.5
Normal Thyroid Clontech A+ 6570-1	34.6	94970_RL_non-Hodgkin's B-cell lymphoma_sscDNA	3.7
Thyroid Cancer GENPAK 064010	23.0	94972_JM1_pre-B-cell lymphoma/leukemia_sscDNA	12.6

Thyroid Cancer INVITROGEN A302152	25.0	94973_Jurkat_T cell leukemia_sscDNA	23.0
Thyroid NAT INVITROGEN A302153	31.4	94974_TF- 1_Erythroleukemia_sscDNA	26.2
Normal Breast GENPAK 061019	30.4	94975_HUT 78_T-cell lymphoma_sscDNA	16.8
84877 Breast Cancer (OD04566)	42.0	94977_U937_Histiocytic lymphoma_sscDNA	26.1
85975 Breast Cancer (OD04590-01)	90.1	94980_KU-812_Myelogenous leukemia_sscDNA	33.9
85976 Breast Cancer Mets (OD04590-03)	87.1	94981_769-P_Clear cell renal carcinoma_sscDNA	15.7
87070 Breast Cancer Metastasis (OD04655-05)	97.9	94983_Caki-2_Clear cell renal carcinoma_sscDNA	19.3
GENPAK Breast Cancer 064006	17.8	94984_SW 839_Clear cell renal carcinoma_sscDNA	21.5
Breast Cancer Res. Gen. 1024	61.1	94986_G401_Wilms' tumor_sscDNA	17.0
Breast Cancer Clontech 9100266	41.8	94987_Hs766T_Pancreatic carcinoma (LN metastasis)_sscDNA	14.1
Breast NAT Clontech 9100265	28.9	94988_CAPAN-1_Pancreatic adenocarcinoma (liver metastasis)_sscDNA	4.8
Breast Cancer INVITROGEN A209073	33.2	94989_SU86.86_Pancreatic carcinoma (liver metastasis)_sscDNA	10.7
Breast NAT INVITROGEN A2090734	33.0	94990_BxPC-3_Pancreatic adenocarcinoma_sscDNA	9.6
Normal Liver GENPAK 061009	13.8	94991_HPAC_Pancreatic adenocarcinoma_sscDNA	13.7
Liver Cancer GENPAK 064003	13.1	94992_MIA PaCa-2_Pancreatic carcinoma_sscDNA	4.0
Liver Cancer Research Genetics RNA 1025	7.7	94993_CFPAC-1_Pancreatic ductal adenocarcinoma_sscDNA	18.7
Liver Cancer Research Genetics RNA 1026	7.9	94994_PANC-1_Pancreatic epithelioid ductal carcinoma_sscDNA	16.8
Paired Liver Cancer Tissue Research Genetics RNA 6004-T	16.8	94996_T24_Bladder carcinma (transitional cell)_sscDNA	14.6
Paired Liver Tissue Research Genetics RNA 6004-N	16.5	94997_5637_Bladder carcinoma_sscDNA	17.0
Paired Liver Cancer Tissue Research Genetics RNA 6005-T	18.4	94998_HT-1197_Bladder carcinoma_sscDNA	10.3
Paired Liver Tissue Research Genetics RNA 6005-N	3.8	94999_UM-UC-3_Bladder carcinma (transitional cell)_sscDNA	8.8
Normal Bladder GENPAK 061001	36.9	95000_A204_Rhabdomyosarco ma_sscDNA	17.6

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Bladder Cancer Research Genetics RNA 1023	16.3	95001_HT-1080_Fibrosarcoma_sscDNA	16.4
Bladder Cancer INVITROGEN A302173	20.2	95002_MG-63_Osteosarcoma (bone)_sscDNA	8.2
87071 Bladder Cancer (OD04718-01)	60.7	95003_SK-LMS-1_Leiomyosarcoma (vulva)_sscDNA	33.7
87072 Bladder Normal Adjacent (OD04718-03)	24.0	95004_SJRH30_Rhabdomyosarcoma (met to bone marrow)_sscDNA	13.4
Normal Ovary Res. Gen.	28.5	95005_A431_Epidermoid carcinoma_sscDNA	6.8
Ovarian Cancer GENPAK 064008	42.0	95007_WM266-4_Melanoma_sscDNA	8.8
87492 Ovary Cancer (OD04768-07)	55.9	95010_DU 145_Prostate carcinoma (brain metastasis)_sscDNA	0.0
87493 Ovary NAT (OD04768-08)	9.2	95012_MDA-MB-468_Breast adenocarcinoma_sscDNA	10.6
Normal Stomach GENPAK 061017	18.0	95013_SCC-4_Squamous cell carcinoma of tongue_sscDNA	0.2
Gastric Cancer Clontech 9060358	9.6	95014_SCC-9_Squamous cell carcinoma of tongue_sscDNA	0.3
NAT Stomach Clontech 9060359	15.5	95015_SCC-15_Squamous cell carcinoma of tongue_sscDNA	0.0
Gastric Cancer Clontech 9060395	21.5	95017_CAL 27_Squamous cell carcinoma of tongue_sscDNA	17.4
NAT Stomach Clontech 9060394	17.2		
Gastric Cancer Clontech 9060397	28.1		
NAT Stomach Clontech 9060396	8.9		
Gastric Cancer GENPAK 064005	36.3		

Table O. Panels 4D and 4.1D

Tissue Name	Relative Expression(%)	Relative Expression(%)
	4.1dx4tm6096t_ag 2835_b2	4Dtm2469f_ag721
93768_Secondary Th1_anti-CD28/anti-CD3	89.8	29.3
93769_Secondary Th2_anti-CD28/anti-CD3	90.4	28.1
93770_Secondary Tr1_anti-CD28/anti-CD3	89.4	27.9
93573_Secondary Th1_resting day 4-6 in IL-2	32.0	10.1
93572_Secondary Th2_resting day 4-6 in IL-2	28.8	6.8
93571_Secondary Tr1_resting day 4-6 in IL-2	32.5	13.5

93568_primary Th1_anti-CD28/anti-CD3	69.4	28.3
93569_primary Th2_anti-CD28/anti-CD3	72.6	28.3
93570_primary Tr1_anti-CD28/anti-CD3	78.5	44.1
93565_primary Th1_resting dy 4-6 in IL-2	24.5	48.3
93566_primary Th2_resting dy 4-6 in IL-2	17.4	26.8
93567_primary Tr1_resting dy 4-6 in IL-2	27.4	23.8
93351_CD45RA CD4 lymphocyte_anti-CD28/anti-CD3	69.5	21.3
93352_CD45RO CD4 lymphocyte_anti-CD28/anti-CD3	62.4	30.8
93251_CD8 Lymphocytes_anti-CD28/anti-CD3	67.5	24.7
93353_chronic CD8 Lymphocytes 2ry_resting dy 4-6 in IL-2	73.9	21.9
93574_chronic CD8 Lymphocytes 2ry_activated CD3/CD28	36.0	16.7
93354_CD4_none	16.1	6.2
93252_Secondary Th1/Th2/Tr1_anti-CD95 CH11	67.3	18.6
93103_LAK cells_resting	41.5	12.5
93788_LAK cells_IL-2	67.4	23.2
93787_LAK cells_IL-2+IL-12	30.1	19.3
93789_LAK cells_IL-2+IFN gamma	29.3	40.6
93790_LAK cells_IL-2+ IL-18	26.4	27.7
93104_LAK cells_PMA/ionomycin and IL-18	17.3	5.5
93578_NK Cells IL-2_resting	63.9	18.8
93109_Mixed Lymphocyte Reaction_Two Way MLR	39.8	18.3
93110_Mixed Lymphocyte Reaction_Two Way MLR	53.2	19.1
93111_Mixed Lymphocyte Reaction_Two Way MLR	45.6	18.6
93112_Mononuclear Cells (PBMCs)_resting	18.2	4.8
93113_Mononuclear Cells (PBMCs)_PWM	35.9	53.6
93114_Mononuclear Cells (PBMCs)_PHA-L	75.5	39.8
93249_Ramos (B cell)_none	63.2	35.8
93250_Ramos (B cell)_ionomycin	80.5	100.0
93349_B lymphocytes_PWM	50.8	82.9
93350_B lymphocytes_CD40L and IL-4	75.0	51.0
92665_EOL-1 (Eosinophil)_dbcAMP differentiated	80.2	27.4
93248_EOL-1 (Eosinophil)_dbcAMP/PMAionomycin	71.6	27.7
93356_Dendritic Cells_none	53.1	24.7
93355_Dendritic Cells_LPS 100 ng/ml	29.2	17.6
93775_Dendritic Cells_anti-CD40	57.9	18.3
93774_Monocytes_resting	28.2	13.0
93776_Monocytes_LPS 50 ng/ml	27.2	7.5
93581_Macrophages_resting	50.6	23.7
93582_Macrophages_LPS 100 ng/ml	15.3	8.8

93098_HUVEC (Endothelial)_none	63.8	48.0
93099_HUVEC (Endothelial)_starved	91.8	82.9
93100_HUVEC (Endothelial)_IL-1b	81.4	26.2
93779_HUVEC (Endothelial)_IFN gamma	92.8	52.1
93102_HUVEC (Endothelial)_TNF alpha + IFN gamma	64.2	26.8
93101_HUVEC (Endothelial)_TNF alpha + IL4	73.0	36.3
93781_HUVEC (Endothelial)_IL-11	78.8	37.4
93583_Lung Microvascular Endothelial Cells_none	100.0	31.4
93584_Lung Microvascular Endothelial Cells_TNFa (4 ng/ml) and IL1b (1 ng/ml)	71.0	26.4
92662_Microvascular Dermal endothelium_none	90.5	47.6
92663_Microvascular Dermal endothelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	45.5	32.1
93773_Bronchial epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml) **	75.7	23.0
93347_Small Airway Epithelium_none	35.4	22.1
93348_Small Airway Epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	49.7	54.0
92668_Coronary Artery SMC_resting	82.5	46.7
92669_Coronary Artery SMC_TNFa (4 ng/ml) and IL1b (1 ng/ml)	60.5	31.9
93107_astrocytes_resting	59.6	34.2
93108_astrocytes_TNFa (4 ng/ml) and IL1b (1 ng/ml)	42.9	25.2
92666_KU-812 (Basophil)_resting	92.8	42.3
92667_KU-812 (Basophil)_PMA/ionoycin	96.0	66.4
93579_CCD1106 (Keratinocytes)_none	80.5	38.4
93580_CCD1106 (Keratinocytes)_TNFa and IFNg **	71.3	12.0
93791_Liver Cirrhosis	18.4	4.0
93792_Lupus Kidney	47.4	4.4
93577_NCI-H292	75.0	47.0
93358_NCI-H292_IL-4	76.8	55.1
93360_NCI-H292_IL-9	60.0	53.6
93359_NCI-H292_IL-13	79.0	33.4
93357_NCI-H292_IFN gamma	72.9	28.5
93777_HPAEC_-	92.8	42.0
93778_HPAEC_IL-1 beta/TNA alpha	87.1	31.0
93254_Normal Human Lung Fibroblast_none	61.8	32.3
93253_Normal Human Lung Fibroblast_TNFa (4 ng/ml) and IL-1b (1 ng/ml)	61.1	14.7
93257_Normal Human Lung Fibroblast_IL-4	76.2	45.7
93256_Normal Human Lung Fibroblast_IL-9	67.4	37.6
93255_Normal Human Lung Fibroblast_IL-13	67.7	32.3
93258_Normal Human Lung Fibroblast_IFN gamma	71.8	46.7

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93106_Dermal Fibroblasts CCD1070_resting	77.1	54.0
93361_Dermal Fibroblasts CCD1070_TNF alpha 4 ng/ml	47.3	61.1
93105_Dermal Fibroblasts CCD1070_IL-1 beta 1 ng/ml	47.9	25.0
93772_dermal fibroblast_IFN gamma	95.6	15.8
93771_dermal fibroblast_IL-4	63.6	37.9
93259_IBD Colitis 1**	9.5	1.2
93260_IBD Colitis 2	28.3	0.9
93261_IBD Crohns	15.0	1.6
735010_Colon_normal	34.4	19.6
735019_Lung_none	63.0	17.4
64028-1_Thymus_none	33.9	26.4
64030-1_Kidney_none	89.8	45.4

Panel 1.2 Summary: The three panels run with three probe/primer sets, two of which are identical, do not concur completely with one another. However, the pattern seen in all three runs is that expression of NOV4a is high in skeletal muscle. Among disease tissues, consistent expression is seen in a lung cancer specimen. Expression of this gene is at lower levels in a variety of other tissues.

Panel 1.3D Summary: NOV4a encodes a protein with a growth factor domain which is expressed in a wide range of tissues and cell types. However, it shows its highest adult expression in the hippocampus (levels are higher in the fetal skeleton) followed by the testes and ovaries. Many growth factors have been shown to be beneficial in the process of compensatory synaptogenesis in the central nervous system in response to injury (in animal models of stroke, head trauma, spinal cord injury). The fact that this gene shows its highest expression in the adult brain suggests that it may have neuroprotective/neurotrophic effects. Furthermore, its specific region of highest expression (the hippocampus) is a site of pronounced neurodegeneration in Alzheimer's disease, and to a lesser extent Parkinson's disease. Therefore, this molecule may be useful as a protein therapeutic in treating these diseases in addition to stroke, head trauma and spinal cord injury. In addition, this gene shows highest expression in fetal skeletal muscle when compared to adult skeletal muscle, potentially indicating a role in tissue regeneration. This is so given that in many instances fetal tissues are rapidly growing and developing whereas adult tissues are in homeostasis.

Panel 2D Summary: The expression of this gene appears to be in virtually all samples in panel 2D. Of particular interest is the observation that there seems to be over-expression of this

gene in samples of gastric and colon cancer relative to their adjacent margins. Thus, therapeutic targeting of this gene may be beneficial in these or other diseases.

Panel 3D Summary: Expression of this gene is seen in almost all tissues and cell lines, except in a few samples of squamous cell carcinoma and prostate carcinoma. It is highest in lung cancers, followed by lower levels in CNS cancers, leiomyosarcoma and leukemias and lymphomas.

Panel 4D and 4.1D Summary: This transcript as probed by Ag721 and Ag2835 is broadly expressed in many tissues and cell types regardless of treatment.

NOV6

Expression of NOV6 was assessed using the primer-probe set Ag274, described in Table P. Results of the RTQ-PCR runs are shown in Tables Q and R.

Table P. Probe Name: Ag274

Primers	Sequences	Length	Start Position
Forward	5'-CAGAACAGATGTATTCCCCTTGGT-3' (SEQ ID NO:85)	24	194
Probe	FAM-5'-CTCAGCGCCTCGATGTCCACCC-3'-TAMRA (SEQ ID NO:86)	22	226
Reverse	5'-CTGGCTTCCCCCAATGC-3' (SEQ ID NO:87)	17	253

Table Q. Panels 2D and 3D

Panel 2D		Panel 3D	
Tissue Name	Rel. Expr., % 2dtm6123f_ag 274	Tissue Name	Rel. Expr., % 3dx4tm6102f_ag274_a2
Normal Colon GENPAK 061003	23.3	94905_Daoy_Medulloblastoma/Cerebellum_sscDNA	14.7
83219 CC Well to Mod Diff (ODO3866)	13.2	94906_TE671_Medulloblastom/Cerebellum_sscDNA	51.2
83220 CC NAT (ODO3866)	10.0	94907_D283 Med_Medulloblastoma/Cerebellum_sscDNA	0.0
83221 CC Gr.2 rectosigmoid	6.0	94908_PFSK-1_Primitive	0.0

(ODO3868)		Neuroectodermal/Cerebellum_s sscDNA	
83222 CC NAT (ODO3868)	6.0	94909_XF-498_CNS_sscDNA	0.0
83235 CC Mod Diff (ODO3920)	3.1	94910_SNB- 78_CNS/glioma_sscDNA	10.5
83236 CC NAT (ODO3920)	10.9	94911_SF- 268_CNS/glioblastoma_sscDN A	0.0
83237 CC Gr.2 ascend colon (ODO3921)	10.2	94912_T98G_Glioblastoma_ssc DNA	10.3
83238 CC NAT (ODO3921)	25.5	96776_SK-N- SH_Neuroblastoma (metastasis)_sscDNA	10.5
83241 CC from Partial Hepatectomy (ODO4309)	9.7	94913_SF- 295_CNS/glioblastoma_sscDN A	0.0
83242 Liver NAT (ODO4309)	48.3	94914_Cerebellum_sscDNA	22.7
87472 Colon mets to lung (OD04451-01)	14.4	96777_Cerebellum_sscDNA	9.0
87473 Lung NAT (OD04451- 02)	17.8	94916_NCI- H292_Mucoepidermoid lung carcinoma_sscDNA	0.0
Normal Prostate Clontech A+ 6546-1	11.0	94917_DMS-114_Small cell lung cancer_sscDNA	6.4
84140 Prostate Cancer (OD04410)	9.7	94918_DMS-79_Small cell lung cancer/neuroendocrine_sscDN A	32.9
84141 Prostate NAT (OD04410)	4.1	94919_NCI-H146_Small cell lung cancer/neuroendocrine_sscDN A	0.0
87073 Prostate Cancer (OD04720-01)	2.0	94920_NCI-H526_Small cell lung cancer/neuroendocrine_sscDN A	11.3
87074 Prostate NAT (OD04720-02)	4.4	94921_NCI-N417_Small cell lung cancer/neuroendocrine_sscDN A	0.0
Normal Lung GENPAK 061010	66.0	94923_NCI-H82_Small cell lung cancer/neuroendocrine_sscDN A	5.0
83239 Lung Met to Muscle (ODO4286)	100.0	94924_NCI-H157_Squamous cell lung cancer (metastasis)_sscDNA	0.0
83240 Muscle NAT (ODO4286)	72.2	94925_NCI-H1155_Large cell lung cancer/neuroendocrine_sscDN A	25.2

84136 Lung Malignant Cancer (OD03126)	35.4	94926_NCI-H1299_Large cell lung cancer/neuroendocrine_sscDNA A	0.0
84137 Lung NAT (OD03126)	68.3	94927_NCI-H727_Lung carcinoid_sscDNA	0.0
84871 Lung Cancer (OD04404)	29.5	94928_NCI-UMC-11_Lung carcinoid_sscDNA	11.5
84872 Lung NAT (OD04404)	35.6	94929_LX-1_Small cell lung cancer_sscDNA	49.9
84875 Lung Cancer (OD04565)	12.4	94930_Colo-205_Colon cancer_sscDNA	0.0
84876 Lung NAT (OD04565)	36.1	94931_KM12_Colon cancer_sscDNA	22.7
85950 Lung Cancer (OD04237- 01)	18.6	94932_KM20L2_Colon cancer_sscDNA	0.0
85970 Lung NAT (OD04237- 02)	22.4	94933_NCI-H716_Colon cancer_sscDNA	0.0
83255 Ocular Mel Met to Liver (ODO4310)	4.2	94935_SW-48_Colon adenocarcinoma_sscDNA	9.7
83256 Liver NAT (ODO4310)	24.3	94936_SW1116_Colon adenocarcinoma_sscDNA	6.1
84139 Melanoma Mets to Lung (OD04321)	5.8	94937_LS 174T_Colon adenocarcinoma_sscDNA	0.0
84138 Lung NAT (OD04321)	29.7	94938_SW-948_Colon adenocarcinoma_sscDNA	7.5
Normal Kidney GENPAK 061008	12.2	94939_SW-480_Colon adenocarcinoma_sscDNA	0.0
83786 Kidney Ca, Nuclear grade 2 (OD04338)	16.5	94940_NCI-SNU-5_Gastric carcinoma_sscDNA	0.0
83787 Kidney NAT (OD04338)	6.2	94941_KATO III_Gastric carcinoma_sscDNA	66.1
83788 Kidney Ca Nuclear grade 1/2 (OD04339)	23.2	94943_NCI-SNU-16_Gastric carcinoma_sscDNA	0.0
83789 Kidney NAT (OD04339)	4.6	94944_NCI-SNU-1_Gastric carcinoma_sscDNA	6.3
83790 Kidney Ca, Clear cell type (OD04340)	11.8	94946_RF-1_Gastric adenocarcinoma_sscDNA	5.5
83791 Kidney NAT (OD04340)	5.8	94947_RF-48_Gastric adenocarcinoma_sscDNA	10.4
83792 Kidney Ca, Nuclear grade 3 (OD04348)	56.6	96778_MKN-45_Gastric carcinoma_sscDNA	0.0
83793 Kidney NAT (OD04348)	22.8	94949_NCI-N87_Gastric carcinoma_sscDNA	11.2
87474 Kidney Cancer (OD04622-01)	24.0	94951_OVCAR-5_Ovarian carcinoma_sscDNA	8.8
87475 Kidney NAT (OD04622-03)	2.6	94952_RL95-2_Uterine carcinoma_sscDNA	0.0
85973 Kidney Cancer (OD04450-01)	0.9	94953_HelaS3_Cervical adenocarcinoma_sscDNA	3.4
85974 Kidney NAT	2.6	94954_Ca Ski_Cervical	4.3

(OD04450-03)		epidermoid carcinoma (metastasis)_sscDNA	
Kidney Cancer Clontech 8120607	5.7	94955_ES-2_Ovarian clear cell carcinoma_sscDNA	9.8
Kidney NAT Clontech 8120608	3.6	94957_Ramos/6h stim_"; Stimulated with PMA/ionomycin 6h_sscDNA	5.6
Kidney Cancer Clontech 8120613	5.7	94958_Ramos/14h stim_"; Stimulated with PMA/ionomycin 14h_sscDNA	100.0
Kidney NAT Clontech 8120614	3.5	94962_MEG-01_Chronic myelogenous leukemia (megokaryoblast)_sscDNA	11.3
Kidney Cancer Clontech 9010320	61.1	94963_Raji_Burkitt's lymphoma_sscDNA	5.4
Kidney NAT Clontech 9010321	24.1	94964_Daudi_Burkitt's lymphoma_sscDNA	5.1
Normal Uterus GENPAK 061018	5.4	94965_U266_B-cell plasmacytoma/myeloma_sscDN A	7.5
Uterus Cancer GENPAK 064011	5.1	94968_CA46_Burkitt's lymphoma_sscDNA	0.0
Normal Thyroid Clontech A+ 6570-1	5.9	94970_RL_non-Hodgkin's B-cell lymphoma_sscDNA	0.0
Thyroid Cancer GENPAK 064010	3.1	94972_JM1_pre-B-cell lymphoma/leukemia_sscDNA	0.0
Thyroid Cancer INVITROGEN A302152	3.3	94973_Jurkat_T cell leukemia_sscDNA	0.0
Thyroid NAT INVITROGEN A302153	13.5	94974_TF-1_Erythroleukemia_sscDNA	0.0
Normal Breast GENPAK 061019	13.2	94975_HUT 78_T-cell lymphoma_sscDNA	14.9
84877 Breast Cancer (OD04566)	40.9	94977_U937_Histiocytic lymphoma_sscDNA	9.1
85975 Breast Cancer (OD04590-01)	29.5	94980_KU-812_Myelogenous leukemia_sscDNA	39.6
85976 Breast Cancer Mets (OD04590-03)	26.1	94981_769-P_Clear cell renal carcinoma_sscDNA	6.0
87070 Breast Cancer Metastasis (OD04655-05)	31.9	94983_Caki-2_Clear cell renal carcinoma_sscDNA	9.7
GENPAK Breast Cancer 064006	16.0	94984_SW 839_Clear cell renal carcinoma_sscDNA	16.4
Breast Cancer Res. Gen. 1024	11.3	94986_G401_Wilms' tumor_sscDNA	6.7
Breast Cancer Clontech 9100266	3.7	94987_Hs766T_Pancreatic carcinoma (LN metastasis)_sscDNA	0.0
Breast NAT Clontech 9100265	4.7	94988_CAPAN-1_Pancreatic adenocarcinoma (liver metastasis)_sscDNA	11.4
Breast Cancer INVITROGEN	5.7	94989_SU86.86_Pancreatic	0.0

A209073		carcinoma (liver metastasis)_sscDNA	
Breast NAT INVITROGEN A2090734	1.5	94990_BxPC-3_Pancreatic adenocarcinoma_sscDNA	0.0
Normal Liver GENPAK 061009	8.4	94991_HPAC_Pancreatic adenocarcinoma_sscDNA	0.0
Liver Cancer GENPAK 064003	8.4	94992_MIA PaCa-2_Pancreatic carcinoma_sscDNA	4.5
Liver Cancer Research Genetics RNA 1025	25.3	94993_CFPAC-1_Pancreatic ductal adenocarcinoma_sscDNA	7.4
Liver Cancer Research Genetics RNA 1026	6.4	94994_PANC-1_Pancreatic epithelioid ductal carcinoma_sscDNA	58.7
Paired Liver Cancer Tissue Research Genetics RNA 6004-T	40.1	94996_T24_Bladder carcinoma (transitional cell)_sscDNA	0.0
Paired Liver Tissue Research Genetics RNA 6004-N	17.8	94997_5637_Bladder carcinoma_sscDNA	11.2
Paired Liver Cancer Tissue Research Genetics RNA 6005-T	10.2	94998_HT-1197_Bladder carcinoma_sscDNA	0.0
Paired Liver Tissue Research Genetics RNA 6005-N	18.6	94999_UM-UC-3_Bladder carcinoma (transitional cell)_sscDNA	10.9
Normal Bladder GENPAK 061001	60.7	95000_A204_Rhabdomyosarcoma_sscDNA	0.0
Bladder Cancer Research Genetics RNA 1023	5.1	95001_HT-1080_Fibrosarcoma_sscDNA	0.0
Bladder Cancer INVITROGEN A302173	18.6	95002_MG-63_Osteosarcoma (bone)_sscDNA	9.9
87071 Bladder Cancer (OD04718-01)	28.5	95003_SK-LMS-1_Leiomyosarcoma (vulva)_sscDNA	0.0
87072 Bladder Normal Adjacent (OD04718-03)	48.6	95004_SJRH30_Rhabdomyosarcoma (met to bone marrow)_sscDNA	3.8
Normal Ovary Res. Gen.	0.0	95005_A431_Epidermoid carcinoma_sscDNA	0.0
Ovarian Cancer GENPAK 064008	16.2	95007_WM266-4_Melanoma_sscDNA	0.0
87492 Ovary Cancer (OD04768-07)	16.4	95010_DU 145_Prostate carcinoma (brain metastasis)_sscDNA	5.5
87493 Ovary NAT (OD04768-08)	19.2	95012_MDA-MB-468_Breast adenocarcinoma_sscDNA	10.8
Normal Stomach GENPAK 061017	6.4	95013_SCC-4_Squamous cell carcinoma of tongue_sscDNA	0.0
Gastric Cancer Clontech 9060358	2.0	95014_SCC-9_Squamous cell carcinoma of tongue_sscDNA	0.0
NAT Stomach Clontech 9060359	5.1	95015_SCC-15_Squamous cell carcinoma of tongue_sscDNA	0.0
Gastric Cancer Clontech	8.4	95017_CAL 27_Squamous cell	0.0

9060395	carcinoma of tongue_sscDNA
NAT Stomach Clontech	10.2
9060394	
Gastric Cancer Clontech	17.4
9060397	
NAT Stomach Clontech	5.3
9060396	
Gastric Cancer GENPAK	14.7
064005	

Table R. Panel 4D

Tissue Name	Rel. Expr., % 4dx4tm5043f_ ag274_b2	Rel. Expr., % 4dx4tm5056f_ ag274_b2
93768_Secondary Th1_anti-CD28/anti-CD3	0.0	0.0
93769_Secondary Th2_anti-CD28/anti-CD3	0.4	0.0
93770_Secondary Tr1_anti-CD28/anti-CD3	0.2	0.2
93573_Secondary Th1_resting day 4-6 in IL-2	0.0	0.0
93572_Secondary Th2_resting day 4-6 in IL-2	0.9	0.0
93571_Secondary Tr1_resting day 4-6 in IL-2	0.3	0.0
93568_primary Th1_anti-CD28/anti-CD3	0.4	0.0
93569_primary Th2_anti-CD28/anti-CD3	0.3	0.3
93570_primary Tr1_anti-CD28/anti-CD3	0.0	0.0
93565_primary Th1_resting dy 4-6 in IL-2	0.4	0.5
93566_primary Th2_resting dy 4-6 in IL-2	0.6	0.1
93567_primary Tr1_resting dy 4-6 in IL-2	0.0	0.3
93351_CD45RA CD4 lymphocyte_anti-CD28/anti-CD3	0.3	0.2
93352_CD45RO CD4 lymphocyte_anti-CD28/anti-CD3	0.0	0.0
93251_CD8 Lymphocytes_anti-CD28/anti-CD3	0.0	0.0
93353_chronic CD8 Lymphocytes 2ry_resting dy 4-6 in IL-2	0.7	0.0
93574_chronic CD8 Lymphocytes 2ry_activated CD3/CD28	0.0	0.0
93354_CD4_none	0.0	0.8
93252_Secondary Th1/Th2/Tr1_anti-CD95 CH11	0.2	0.0
93103_LAK cells_resting	13.3	12.6
93788_LAK cells_IL-2	0.4	0.4
93787_LAK cells_IL-2+IL-12	0.5	1.6
93789_LAK cells_IL-2+IFN gamma	0.8	0.4
93790_LAK cells_IL-2+ IL-18	0.5	0.4
93104_LAK cells_PMA/ionomycin and IL-18	5.4	6.9
93578_NK Cells IL-2_resting	0.5	0.1
93109_Mixed Lymphocyte Reaction_Two Way MLR	44.4	38.7
93110_Mixed Lymphocyte Reaction_Two Way MLR	8.0	6.9
93111_Mixed Lymphocyte Reaction_Two Way MLR	0.4	0.5
93112_Mononuclear Cells (PBMCs)_resting	1.4	1.6

93113_Mononuclear Cells (PBMCs)_PWM	0.7	0.5
93114_Mononuclear Cells (PBMCs)_PHA-L	2.6	3.2
93249_Ramos (B cell)_none	0.0	0.3
93250_Ramos (B cell)_ionomycin	0.0	0.7
93349_B lymphocytes_PWM	0.0	0.0
93350_B lymphocytes_CD40L and IL-4	0.3	0.6
92665_EOL-1 (Eosinophil)_dbcAMP differentiated	0.2	0.4
93248_EOL-1 (Eosinophil)_dbcAMP/PMAionomycin	0.0	0.3
93356_Dendritic Cells_none	7.9	6.4
93355_Dendritic Cells_LPS 100 ng/ml	32.1	31.6
93775_Dendritic Cells_anti-CD40	3.8	3.6
93774_Monocytes_resting	7.9	8.4
93776_Monocytes_LPS 50 ng/ml	100.0	100.0
93581_Macrophages_resting	3.6	3.5
93582_Macrophages_LPS 100 ng/ml	95.3	88.3
93098_HUVEC (Endothelial)_none	0.2	0.0
93099_HUVEC (Endothelial)_starved	0.4	0.3
93100_HUVEC (Endothelial)_IL-1b	0.5	0.0
93779_HUVEC (Endothelial)_IFN gamma	0.0	0.1
93102_HUVEC (Endothelial)_TNF alpha + IFN gamma	0.3	0.1
93101_HUVEC (Endothelial)_TNF alpha + IL4	0.0	0.2
93781_HUVEC (Endothelial)_IL-11	0.2	0.0
93583_Lung Microvascular Endothelial Cells_none	0.0	0.3
93584_Lung Microvascular Endothelial Cells_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0.0	0.3
92662_Microvascular Dermal endothelium_none	0.0	0.0
92663_Microvascular Dermal endothelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0.0	0.2
93773_Bronchial epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml) **	0.0	0.3
93347_Small Airway Epithelium_none	0.0	0.0
93348_Small Airway Epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0.0	0.1
92668_Coronary Artery SMC_resting	0.2	0.0
92669_Coronary Artery SMC_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0.0	0.0
93107_astrocytes_resting	0.0	0.0
93108_astrocytes_TNFa (4 ng/ml) and IL1b (1 ng/ml)	1.0	0.3
92666_KU-812 (Basophil)_resting	0.0	0.0
92667_KU-812 (Basophil)_PMA/ionomycin	0.4	0.1
93579_CCD1106 (Keratinocytes)_none	0.4	0.0
93580_CCD1106 (Keratinocytes)_TNFa and IFNg **	0.3	0.9
93791_Liver Cirrhosis	2.3	1.5
93792_Lupus Kidney	1.8	0.8

WO 01/90155	PCT/US01/17073	
93577_NCI-H292	0.0	0.4
93358_NCI-H292_IL-4	0.3	0.2
93360_NCI-H292_IL-9	0.0	0.0
93359_NCI-H292_IL-13	0.0	0.2
93357_NCI-H292_IFN gamma	0.0	0.0
93777_HPAEC_-	0.3	0.0
93778_HPAEC_IL-1 beta/TNA alpha	0.0	0.0
93254_Normal Human Lung Fibroblast_none	0.3	0.0
93253_Normal Human Lung Fibroblast_TNFa (4 ng/ml) and IL-1b (1 ng/ml)	0.3	0.0
93257_Normal Human Lung Fibroblast_IL-4	0.4	0.4
93256_Normal Human Lung Fibroblast_IL-9	0.0	0.0
93255_Normal Human Lung Fibroblast_IL-13	0.0	0.0
93258_Normal Human Lung Fibroblast_IFN gamma	0.0	0.3
93106_Dermal Fibroblasts CCD1070_resting	0.7	0.2
93361_Dermal Fibroblasts CCD1070_TNF alpha 4 ng/ml	0.4	0.0
93105_Dermal Fibroblasts CCD1070_IL-1 beta 1 ng/ml	0.0	0.1
93772_dermal fibroblast_IFN gamma	0.0	0.0
93771_dermal fibroblast_IL-4	0.4	0.2
93259_IBD Colitis 1**	1.5	1.6
93260_IBD Colitis 2	0.0	0.2
93261_IBD Crohns	0.6	0.7
735010_Colon_normal	4.1	4.1
735019_Lung_none	7.5	8.0
64028-1_Thymus_none	0.9	0.1
64030-1_Kidney_none	4.8	3.0

Panel 2D Summary: The expression of NOV6 in panel 2D is widespread, as it appears to be expressed in most samples in this panel. Of particular interest is the differential expression of this gene in renal cell carcinoma samples when compared to their normal adjacent tissues. These data indicate that this gene may be of utility as a target for therapeutic intervention in kidney cancers.

Panel 3D Summary: Expression of this gene is highest in the Ramos cell line stimulated with PMA and ionomycin for 16 hrs, followed by lower expression in cell lines derived from gastric carcinoma and pancreatic ductal carcinoma, and lower still in small cell lung carcinoma, medulloblastoma and myelogenous leukemia.

Panel 4D Summary: The expression of NOV6 is limited to LPS activated monocytes and cell types related (macrophages) or derived from monocytes (dendritic cells). The putative sialoadhesin encoded for by this transcript could be utilized as an adhesion molecule for

directing monocyte extravasation into tissues, and as a cell:cell interaction molecule. Protein therapeutics designed from the protein encoded for by this molecule could block monocyte extravasation. Antibody therapeutics could also block extravasation. These therapies could reduce or inhibit inflammation associated with asthma, psoriasis, emphysema, arthritis, and other inflammatory diseases. [Reference: van den Berg et al., J Immunol 2001 Mar 15;166(6):3637-40 Cutting edge: CD43 functions as a T cell counterreceptor for the macrophage adhesion receptor sialoadhesin (Siglec-1). Sialoadhesin (Siglec-1) is a macrophage-restricted sialic acid-binding receptor that mediates interactions with hemopoietic cells, including lymphocytes. In this study, we identify sialoadhesin counterreceptors on T lymphocytes. Several major glycoproteins (85, 130, 240 kDa) were precipitated by sialoadhesin-Fc fusion proteins from a murine T cell line (TK-1). Binding of sialoadhesin to these glycoproteins was sialic acid dependent and was abolished by mutation of a critical residue (R97A) of the sialic acid binding site in the membrane distal Ig-like domain of sialoadhesin. The 130- and 240-kDa sialoadhesin-binding glycoproteins were identified as the sialomucins CD43 and P-selectin glycoprotein ligand 1 (CD162), respectively. CD43 expressed in COS cells supported increased binding to immobilized sialoadhesin. Finally, sialoadhesin bound different glycoforms of CD43 expressed in Chinese hamster ovary cells, including unbranched (core 1) and branched (core 2) O-linked glycans, that are normally found on CD43 in resting and activated T cells, respectively. These results identify CD43 as a T cell counterreceptor for sialoadhesin and suggest that in addition to its anti-adhesive role CD43 may promote cell-cell interactions.]

NOV7

Expression of NOV7 was assessed using the primer-probe set Ag582, described in Table S. Results of the RTQ-PCR runs are shown in Table T, U and V.

Table S. Probe Name: Ag582

Forward	5'-AGGCTGTAGATAAAGGGGTTCA-3' (SEQ ID NO: 88)	59.2	22	76
Probe	TET-5'-TGAGAGCCACAATGACATCCTTGTC-3' - TAMRA (SEQ ID NO: 89)	69.1	26	122
Reverse	5'-TTCCCGACTGTAAGCAGTTCTA-3' (SEQ ID NO: 90)	59	22	149
Forward	5'-AGGCTGTAGATAAAGGGGTTCA-3' (SEQ ID NO: 91)	59.2	22	76

Table T. Panel 1.1

Tissue Name	Rel. Expr., % 1.1tm754f_ag5	Rel. Expr., % 1.1tm855f_ag5
	82	82
Adipose	0.0	0.0
Adrenal gland	0.0	0.0
Bladder	37.6	1.7
Brain (amygdala)	0.0	0.0
Brain (cerebellum)	15.7	17.7
Brain (hippocampus)	0.0	0.0
Brain (substantia nigra)	4.4	4.4
Brain (thalamus)	0.0	0.0
Cerebral Cortex	0.4	0.2
Brain (fetal)	9.2	15.3
Brain (whole)	0.4	3.3
CNS ca. (glio/astro) U-118-MG	6.7	8.7
CNS ca. (astro) SF-539	0.0	2.6
CNS ca. (astro) SNB-75	3.3	5.3
CNS ca. (astro) SW1783	9.5	5.6
CNS ca. (glio) U251	7.2	3.8
CNS ca. (glio) SF-295	33.2	33.9
CNS ca. (glio) SNB-19	21.3	15.3
CNS ca. (glio/astro) U87-MG	11.0	11.3
CNS ca.* (neuro; met) SK-N-AS	3.1	2.7
Mammary gland	0.0	0.0
Breast ca. BT-549	7.3	4.2
Breast ca. MDA-N	3.1	2.9
Breast ca.* (pl. effusion) T47D	3.7	4.0
Breast ca.* (pl. effusion) MCF-7	6.3	3.6
Breast ca.* (pl.ef) MDA-MB-231	10.7	14.2
Small intestine	0.1	0.0
Colorectal	0.0	0.0
Colon ca. HT29	5.3	2.8
Colon ca. CaCo-2	2.5	0.2
Colon ca. HCT-15	0.4	0.0
Colon ca. HCT-116	1.4	1.3
Colon ca. HCC-2998	14.3	15.3
Colon ca. SW480	0.3	0.0
Colon ca.* (SW480 met)SW620	17.3	9.5
Stomach	0.0	0.0
Gastric ca.* (liver met) NCI-N87	18.8	10.2
Heart	0.2	2.2
Fetal Skeletal	7.6	6.3
Skeletal muscle	0.0	0.0
Endothelial cells	5.6	0.0
Endothelial cells (treated)	0.0	0.0
Kidney	0.0	0.0
Kidney (fetal)	0.0	0.4

Renal ca.	786-0	26.2	16.7
Renal ca.	A498	29.7	0.0
Renal ca.	ACHN	0.7	20.2
Renal ca.	TK-10	22.4	17.0
Renal ca.	UO-31	59.0	20.3
Renal ca.	RXF 393	12.3	5.8
Liver		0.0	0.0
Liver (fetal)		0.0	0.0
Liver ca. (hepatoblast) HepG2		1.6	0.3
Lung		0.0	0.0
Lung (fetal)		0.0	0.0
Lung ca (non-s.cell) HOP-62		100.0	100.0
Lung ca. (large cell) NCI-H460		24.7	16.8
Lung ca. (non-s.cell) NCI-H23		5.0	2.0
Lung ca. (non-s.cl) NCI-H522		20.2	16.7
Lung ca. (non-sm. cell) A549		14.9	8.7
Lung ca. (s.cell var.) SHP-77		2.6	0.6
Lung ca. (small cell) LX-1		13.8	10.2
Lung ca. (small cell) NCI-H69		1.1	3.4
Lung ca. (squam.) SW 900		53.6	45.7
Lung ca. (squam.) NCI-H596		18.3	9.0
Lymph node		0.0	0.0
Spleen		0.0	0.0
Thymus		0.0	0.0
Ovary		0.0	0.0
Ovarian ca.	IGROV-1	28.9	6.1
Ovarian ca.	OVCAR-3	12.6	0.5
Ovarian ca.	OVCAR-4	1.4	0.9
Ovarian ca.	OVCAR-5	36.3	28.7
Ovarian ca.	OVCAR-8	17.6	17.1
Ovarian ca.* (ascites) SK-OV-3		23.3	19.5
Pancreas		0.0	0.0
Pancreatic ca.	CAPAN 2	0.6	2.9
Pituitary gland		2.1	1.5
Placenta		2.3	0.0
Prostate		0.0	1.7
Prostate ca.* (bone met) PC-3		8.0	6.7
Salivary gland		0.0	0.0
Trachea		0.0	0.0
Spinal cord		1.4	0.0
Testis		0.0	0.0
Thyroid		0.0	0.0
Uterus		0.6	1.0
Melanoma	M14	0.0	1.2
Melanoma	LOX IMVI	12.3	7.5
Melanoma	UACC-62	0.4	1.4
Melanoma	SK-MEL-28	27.7	26.2
Melanoma* (met) SK-MEL-5		13.1	17.3
Melanoma	Hs688(A).T	8.1	9.2

Table U. Panel 2D

Tissue Name	Rel. Expr., % 2dtm2899f_ag5	Tissue Name	Rel. Expr., % 2dtm2899f_ag5
	82		82
Normal Colon GENPAK 061003	68.3	Kidney NAT Clontech 8120608	1.2
83219 CC Well to Mod Diff (ODO3866)	24.1	Kidney Cancer Clontech 8120613	3.3
83220 CC NAT (ODO3866)	8.0	Kidney NAT Clontech 8120614	1.1
83221 CC Gr.2 rectosigmoid (ODO3868)	23.0	Kidney Cancer Clontech 9010320	32.5
83222 CC NAT (ODO3868)	6.5	Kidney NAT Clontech 9010321	16.3
83235 CC Mod Diff (ODO3920)	62.0	Normal Uterus GENPAK 061018	11.0
83236 CC NAT (ODO3920)	15.7	Uterus Cancer GENPAK 064011	13.1
83237 CC Gr.2 ascend colon (ODO3921)	23.2	Normal Thyroid Clontech A+ 6570-1	1.6
83238 CC NAT (ODO3921)	2.7	Thyroid Cancer GENPAK 064010	8.7
83241 CC from Partial Hepatectomy (ODO4309)	11.2	Thyroid Cancer INVITROGEN A302152	2.5
83242 Liver NAT (ODO4309)	9.3	Thyroid NAT INVITROGEN A302153	1.1
87472 Colon mets to lung (OD04451-01)	8.2	Normal Breast GENPAK 061019	12.1
87473 Lung NAT (OD04451-02)	9.9	84877 Breast Cancer (OD04566)	4.2
Normal Prostate Clontech A+ 6546-1	21.8	85975 Breast Cancer (OD04590-01)	49.0
84140 Prostate Cancer (OD04410)	40.9	85976 Breast Cancer Mets (OD04590-03)	32.5
84141 Prostate NAT (OD04410)	31.4	87070 Breast Cancer Metastasis (OD04655-05)	28.3
87073 Prostate Cancer (OD04720-01)	21.6	GENPAK Breast Cancer 064006	24.8
87074 Prostate NAT (OD04720-02)	24.0	Breast Cancer Res. Gen. 1024	40.1
Normal Lung GENPAK 061010	28.5	Breast Cancer Clontech 9100266	28.5
83239 Lung Met to Muscle (ODO4286)	8.8	Breast NAT Clontech 9100265	10.5
83240 Muscle NAT (ODO4286)	11.7	Breast Cancer INVITROGEN A209073	13.5
84136 Lung Malignant Cancer (OD03126)	6.8	Breast NAT INVITROGEN A2090734	0.9
84137 Lung NAT (OD03126)	10.5	Normal Liver GENPAK 061009	3.2
		235	

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84871 Lung Cancer (OD04404)	6.1	Liver Cancer GENPAK 064003	13.0
84872 Lung NAT (OD04404)	18.4	Liver Cancer Research Genetics RNA 1025	3.2
84875 Lung Cancer (OD04565)	55.9	Liver Cancer Research Genetics RNA 1026	2.6
84876 Lung NAT (OD04565)	10.7	Paired Liver Cancer Tissue Research Genetics RNA 6004-T	7.2
85950 Lung Cancer (OD04237-01)	91.4	Paired Liver Tissue Research Genetics RNA 6004-N	15.8
85970 Lung NAT (OD04237-02)	19.8	Paired Liver Cancer Tissue Research Genetics RNA 6005-T	0.5
83255 Ocular Mel Met to Liver (ODO4310)	2.9	Paired Liver Tissue Research Genetics RNA 6005-N	0.0
83256 Liver NAT (ODO4310)	7.6	Normal Bladder GENPAK 061001	21.8
84139 Melanoma Mets to Lung (OD04321)	6.2	Bladder Cancer Research Genetics RNA 1023	13.2
84138 Lung NAT (OD04321)	15.0	Bladder Cancer INVITROGEN A302173	5.5
Normal Kidney GENPAK 061008	11.8	87071 Bladder Cancer (OD04718-01)	46.0
83786 Kidney Ca, Nuclear grade 2 (OD04338)	17.4	87072 Bladder Normal Adjacent (OD04718-03)	16.3
83787 Kidney NAT (OD04338)	5.5	Normal Ovary Res. Gen.	2.5
83788 Kidney Ca Nuclear grade 1/2 (OD04339)	54.0	Ovarian Cancer GENPAK 064008	7.7
83789 Kidney NAT (OD04339)	11.1	87492 Ovary Cancer (OD04768-07)	19.8
83790 Kidney Ca, Clear cell type (OD04340)	100.0	87493 Ovary NAT (OD04768-08)	7.2
83791 Kidney NAT (OD04340)	12.2	Normal Stomach GENPAK 061017	29.7
83792 Kidney Ca, Nuclear grade 3 (OD04348)	35.6	Gastric Cancer Clontech 9060358	1.8
83793 Kidney NAT (OD04348)	14.9	NAT Stomach Clontech 9060359	2.0
87474 Kidney Cancer (OD04622-01)	6.3	Gastric Cancer Clontech 9060395	1.9
87475 Kidney NAT (OD04622-03)	2.3	NAT Stomach Clontech 9060394	3.5
85973 Kidney Cancer (OD04450-01)	24.0	Gastric Cancer Clontech 9060397	5.5
85974 Kidney NAT (OD04450-03)	8.2	NAT Stomach Clontech 9060396	1.5
Kidney Cancer Clontech 8120607	0.0	Gastric Cancer GENPAK 064005	9.7

Table V. Panel 4D

Tissue Name	Rel. Expr., % 4dtm2938f_ag5	Rel. Expr., % 4dx4tm5034f_a g582_a1
	82	
93768_Secondary Th1_anti-CD28/anti-CD3	13.7	3.2
93769_Secondary Th2_anti-CD28/anti-CD3	7.1	1.0
93770_Secondary Tr1_anti-CD28/anti-CD3	12.9	3.8
93573_Secondary Th1_resting day 4-6 in IL-2	1.7	0.0
93572_Secondary Th2_resting day 4-6 in IL-2	3.2	4.3
93571_Secondary Tr1_resting day 4-6 in IL-2	2.2	2.6
93568_primary Th1_anti-CD28/anti-CD3	4.9	2.8
93569_primary Th2_anti-CD28/anti-CD3	1.1	4.0
93570_primary Tr1_anti-CD28/anti-CD3	6.6	4.4
93565_primary Th1_resting dy 4-6 in IL-2	0.0	6.2
93566_primary Th2_resting dy 4-6 in IL-2	0.0	7.2
93567_primary Tr1_resting dy 4-6 in IL-2	1.2	2.3
93351_CD45RA CD4 lymphocyte_anti-CD28/anti-CD3	55.9	12.5
93352_CD45RO CD4 lymphocyte_anti-CD28/anti-CD3	15.5	1.3
93251_CD8 Lymphocytes_anti-CD28/anti-CD3	0.0	0.7
93353_chronic CD8 Lymphocytes 2ry_resting dy 4-6 in IL-2	0.0	0.0
93574_chronic CD8 Lymphocytes 2ry_activated CD3/CD28	4.7	0.0
93354_CD4_none	0.6	0.0
93252_Secondary Th1/Th2/Tr1_anti-CD95 CH11	4.2	3.7
93103_LAK cells_resting	7.7	2.3
93788_LAK cells_IL-2	3.0	7.6
93787_LAK cells_IL-2+IL-12	1.7	1.7
93789_LAK cells_IL-2+IFN gamma	0.0	4.0
93790_LAK cells_IL-2+ IL-18	0.0	6.8
93104_LAK cells_PMA/ionomycin and IL-18	20.4	16.6
93578_NK Cells IL-2_resting	0.9	4.1
93109_Mixed Lymphocyte Reaction_Two Way MLR	9.2	5.7
93110_Mixed Lymphocyte Reaction_Two Way MLR	2.1	3.9
93111_Mixed Lymphocyte Reaction_Two Way MLR	2.5	0.0
93112_Mononuclear Cells (PBMCs)_resting	4.0	5.6
93113_Mononuclear Cells (PBMCs)_PWM	2.4	5.8
93114_Mononuclear Cells (PBMCs)_PHA-L	3.4	10.1
93249_Ramos (B cell)_none	0.0	0.0
93250_Ramos (B cell)_ionomycin	0.8	2.0
93349_B lymphocytes_PWM	2.4	15.1
93350_B lymphocytes_CD40L and IL-4	6.4	17.4
92665_EOL-1 (Eosinophil)_dbcAMP differentiated	20.0	5.8
93248_EOL-1 (Eosinophil)_dbcAMP/PMAionomycin	5.7	3.1

93356_Dendritic Cells_none	8.8	8.0
93355_Dendritic Cells_LPS 100 ng/ml	6.8	8.4
93775_Dendritic Cells_anti-CD40	6.5	10.6
93774_Monocytes_resting	20.6	21.7
93776_Monocytes_LPS 50 ng/ml	12.2	11.4
93581_Macrophages_resting	7.5	19.2
93582_Macrophages_LPS 100 ng/ml	2.2	6.4
93098_HUVEC (Endothelial)_none	5.3	11.2
93099_HUVEC (Endothelial)_starved	7.4	41.9
93100_HUVEC (Endothelial)_IL-1b	8.2	10.0
93779_HUVEC (Endothelial)_IFN gamma	100.0	7.2
93102_HUVEC (Endothelial)_TNF alpha + IFN gamma	60.3	38.1
93101_HUVEC (Endothelial)_TNF alpha + IL4	33.9	32.6
93781_HUVEC (Endothelial)_IL-11	15.4	8.0
93583_Lung Microvascular Endothelial Cells_none	21.2	26.4
93584_Lung Microvascular Endothelial Cells_TNFa (4 ng/ml) and IL1b (1 ng/ml)	37.1	65.7
92662_Microvascular Dermal endothelium_none	26.6	34.5
92663_Microvascular Dermal endothelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	19.6	42.8
93773_Bronchial epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml) **	8.6	22.5
93347_Small Airway Epithelium_none	6.9	10.6
93348_Small Airway Epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	12.9	44.3
92668_Coronary Artery SMC_resting	8.8	8.9
92669_Coronary Artery SMC_TNFa (4 ng/ml) and IL1b (1 ng/ml)	21.0	4.1
93107_astrocytes_resting	59.9	32.8
93108_astrocytes_TNFa (4 ng/ml) and IL1b (1 ng/ml)	38.4	19.2
92666_KU-812 (Basophil)_resting	3.3	0.0
92667_KU-812 (Basophil)_PMA/ionoycin	3.3	8.9
93579_CCD1106 (Keratinocytes)_none	8.4	12.5
93580_CCD1106 (Keratinocytes)_TNFa and IFNg **	39.0	6.1
93791_Liver Cirrhosis	7.7	11.9
93792_Lupus Kidney	2.0	11.6
93577_NCI-H292	15.6	15.5
93358_NCI-H292_IL-4	18.2	31.0
93360_NCI-H292_IL-9	5.5	30.7
93359_NCI-H292_IL-13	32.8	10.2
93357_NCI-H292_IFN gamma	28.1	14.6
93777_HPAEC_-	31.6	15.4
93778_HPAEC_IL-1 beta/TNA alpha	20.2	29.9
93254_Normal Human Lung Fibroblast_none	21.5	20.4

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93253_Normal Human Lung Fibroblast_TNF α (4 ng/ml) and IL-1b (1 ng/ml)	4.4	8.8
93257_Normal Human Lung Fibroblast_IL-4	33.2	35.1
93256_Normal Human Lung Fibroblast_IL-9	26.6	54.1
93255_Normal Human Lung Fibroblast_IL-13	25.9	55.3
93258_Normal Human Lung Fibroblast_IFN gamma	17.6	38.4
93106_Dermal Fibroblasts CCD1070_resting	28.1	77.0
93361_Dermal Fibroblasts CCD1070_TNF alpha 4 ng/ml	30.1	100.0
93105_Dermal Fibroblasts CCD1070_IL-1 beta 1 ng/ml	10.2	38.1
93772_dermal fibroblast_IFN gamma	25.0	8.8
93771_dermal fibroblast_IL-4	39.5	16.0
93260_IBD Colitis 2	2.0	1.2
93261_IBD Crohns	0.0	0.0
735010_Colon_normal	6.6	2.1
735019_Lung_none	5.4	7.2
64028-1_Thymus_none	8.3	9.9
64030-1_Kidney_none	11.3	21.8

Panel 1.1 Summary: NOV7 is expressed at moderately high levels in the brain, bladder, heart, pituitary and uterus. Notably, its expression is seen to be high in fetal skeletal muscle and absent in adult tissue. Therefore this gene may be used as therapy for tissue regeneration.

- 5 Moreover, this gene is overexpressed in lung cancer, renal cancer, ovarian cancer, CNS cancer, melanoma and breast cancer, with levels in normal tissue being low/undetectable. Therefore, therapies targeted towards this protein may be effective therapeutics in these kinds of cancer.

- 10 *Panel 2D Summary:* Overall, the expression of this gene shows varied expression across panel 2D. However, there appears to be cancer-associated expression in the samples derived from lung, colon and kidney cancers, when compared to their respective normal adjacent tissues. This is consistent with expression in panel 1.1. Thus, targeting of this gene may provide therapeutic utility in these diseases.

Panel 4D Summary: Expression of this gene in the two panels does not replicate very well and therefore no firm conclusions can be drawn.

15 **NOV8a**

Expression of NOV8a was assessed using the primer-probe set Ag850, described in Table W. Results of the RTQ-PCR runs are shown in Table X.

Table W. Probe Name: Ag850

Primers	Sequences	TM	Length	Start Position
Forward	5'-CCTTTCTTCTCTTCCTCCTCAA-3' (SEQ ID NO: 92)	59.1	22	25
Probe	FAM-5'-CACCTGGCGAGTGCTCCTCTCTG-3' -TAMRA (SEQ ID NO: 93)	70	23	71
Reverse	5'-GGTGGATGGCGTTGTAGAG-3' (SEQ ID NO: 94)	59.1	19	96

Table X. Panel 4.1D

Tissue Name	Rel. Expr., % 4.1dx4tm6089f _ag850_b2	Tissue Name	Rel. Expr., % 4.1dx4tm6089f _ag850_b2
93768_Secondary Th1_anti- CD28/anti-CD3	0.0	93100_HUVEC (Endothelial)_IL-1b	0.0
93769_Secondary Th2_anti- CD28/anti-CD3	0.0	93779_HUVEC (Endothelial)_IFN gamma	0.8
93770_Secondary Tr1_anti- CD28/anti-CD3	0.0	93102_HUVEC (Endothelial)_TNF alpha + IFN gamma	1.0
93573_Secondary Th1_resting day 4-6 in IL-2	0.0	93101_HUVEC (Endothelial)_TNF alpha + IL4	0.0
93572_Secondary Th2_resting day 4-6 in IL-2	0.0	93781_HUVEC (Endothelial)_IL-11	0.0
93571_Secondary Tr1_resting day 4-6 in IL-2	0.7	93583_Lung Microvascular Endothelial Cells_none	0.0
93568_primary Th1_anti- CD28/anti-CD3	0.2	93584_Lung Microvascular Endothelial Cells_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0.0
93569_primary Th2_anti- CD28/anti-CD3	0.0	92662_Microvascular Dermal endothelium_none	0.3
93570_primary Tr1_anti- CD28/anti-CD3	0.6	92663_Microsvascular Dermal endothelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0.0
93565_primary Th1_resting dy 4-6 in IL-2	0.0	93773_Bronchial epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml) **	0.9
93566_primary Th2_resting dy 4-6 in IL-2	0.0	93347_Small Airway Epithelium_none	1.8
93567_primary Tr1_resting dy 4-6 in IL-2	0.0	93348_Small Airway Epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	4.0
93351_CD45RA CD4 lymphocyte_anti-CD28/anti- CD3	7.4	92668_Coronary Artery SMC_resting	1.8
93352_CD45RO CD4 lymphocyte_anti-CD28/anti-	0.2	92669_Coronary Artery SMC TNFa (4 ng/ml) and IL1b	1.3

CD3		(1 ng/ml)	
93251_CD8 Lymphocytes_anti-CD28/anti-CD3	0.0	93107_astrocytes_resting	31.9
93353_chronic CD8 Lymphocytes 2ry_resting dy 4-6 in IL-2	0.2	93108_astrocytes_TNFa (4 ng/ml) and IL1b (1 ng/ml)	33.4
93574_chronic CD8 Lymphocytes 2ry_activated CD3/CD28	0.3	92666_KU-812 (Basophil)_resting	0.0
93354_CD4_none	0.0	92667_KU-812 (Basophil)_PMA/ionoycin	0.0
93252_Secondary Th1/Th2/Tr1_anti-CD95 CH11	0.1	93579_CCD1106 (Keratinocytes)_none	0.0
93103_LAK cells_resting	0.0	93580_CCD1106 (Keratinocytes)_TNFa and IFNg **	0.0
93788_LAK cells_IL-2	0.0	93791_Liver Cirrhosis	1.0
93787_LAK cells_IL-2+IL-12	0.0	93577_NCI-H292	2.2
93789_LAK cells_IL-2+IFN gamma	0.0	93358_NCI-H292_IL-4	1.1
93790_LAK cells_IL-2+ IL-18	0.0	93360_NCI-H292_IL-9	1.5
93104_LAK cells_PMA/ionomycin and IL-18	0.6	93359_NCI-H292_IL-13	0.9
93578_NK Cells IL-2_resting	0.0	93357_NCI-H292_IFN gamma	0.3
93109_Mixed Lymphocyte Reaction_Two Way MLR	0.0	93777_HPAEC_-	0.0
93110_Mixed Lymphocyte Reaction_Two Way MLR	0.0	93778_HPAEC_IL-1 beta/TNA alpha	0.0
93111_Mixed Lymphocyte Reaction_Two Way MLR	0.2	93254_Normal Human Lung Fibroblast_none	0.0
93112_Mononuclear Cells (PBMCs)_resting	0.0	93253_Normal Human Lung Fibroblast_TNFa (4 ng/ml) and IL-1b (1 ng/ml)	0.0
93113_Mononuclear Cells (PBMCs)_PWM	0.0	93257_Normal Human Lung Fibroblast_IL-4	0.1
93114_Mononuclear Cells (PBMCs)_PHA-L	0.0	93256_Normal Human Lung Fibroblast_IL-9	0.0
93249_Ramos (B cell)_none	0.0	93255_Normal Human Lung Fibroblast_IL-13	0.1
93250_Ramos (B cell)_ionomycin	0.0	93258_Normal Human Lung Fibroblast_IFN gamma	0.8
93349_B lymphocytes_PWM	0.0	93106_Dermal Fibroblasts CCD1070_resting	14.5
93350_B lymphocytes_CD40L and IL-4	0.1	93361_Dermal Fibroblasts CCD1070_TNF alpha 4 ng/ml	15.2
92665_EOL-1 (Eosinophil)_dbcAMP differentiated	0.0	93105_Dermal Fibroblasts CCD1070_IL-1 beta 1 ng/ml	10.1
93248_EOL-1	0.0	93772_dermal fibroblast_IFN	0.0

(Eosinophil)_dbcAMP/PMAion omycin		gamma	
93356_Dendritic Cells_none	0.0	93771_dermal fibroblast_IL-4	0.0
93355_Dendritic Cells_LPS 100 ng/ml	0.3	93892_Dermal fibroblasts_none	0.0
93775_Dendritic Cells_anti- CD40	0.0	99202_Neutrophils_TNFa+LPS	0.0
93774_Monocytes_resting	0.0	99203_Neutrophils_none	0.0
93776_Monocytes_LPS 50 ng/ml	0.0	735010_Colon_normal	0.6
93581_Macrophages_resting	0.0	735019_Lung_none	0.9
93582_Macrophages_LPS 100 ng/ml	0.8	64028-1_Thymus_none	6.0
93098_HUVEC (Endothelial)_none	0.0	64030-1_Kidney_none	100.0
93099_HUVEC (Endothelial)_starved	0.0		

Panel 4.1D Summary: The NOV8a transcript is highly expressed in normal kidney and astrocytes but not in most other tissues. The expression of this transcript or of the protein it encodes may function as a marker for normal kidney or for astrocytes.

5 NOV8c

Expression of NOV8c was assessed using the primer-probe sets Ag217, described in Table Y. Results of the RTQ-PCR runs are shown in Tables Z and AA.

Table Y. Probe Name: Ag217

Primers	Sequences	TM	Length	Start Position
Forward	5'-ATCTGTGCTGAGGCATGTTCCCT-3' (SEQ ID NO: 95)		22	163
Probe	FAM-5'-ATCCTCCTCCCTCCCCGGCTCTC-3'-TAMRA (SEQ ID NO: 96)		23	192
Reverse	5'-CTGCATGGCTGGTGTGATG-3' (SEQ ID NO: 97)		19	222

Table Z. Panel 1

Tissue Name	Rel. Expr., % tm303f (ag217)	Tissue Name	Rel. Expr., % tm303f (ag217)
Endothelial cells	0.0	Kidney (fetal)	0.0
Endothelial cells (treated)	0.0	Renal ca.	786-0 0.0

Pancreas		0.0	Renal ca.	A498	0.0
Pancreatic ca.	CAPAN 2	5.4	Renal ca.	RXF 393	0.0
Adipose		0.0	Renal ca.	ACHN	0.0
Adrenal gland		0.0	Renal ca.	UO-31	0.0
Thyroid		0.0	Renal ca.	TK-10	0.0
Salivary gland		0.0	Liver		0.0
Pituitary gland		0.0	Liver (fetal)		0.0
Brain (fetal)		0.0	Liver ca. (hepatoblast)	HepG2	0.0
Brain (whole)		0.0	Lung		0.0
Brain (amygdala)		0.0	Lung (fetal)		0.0
Brain (cerebellum)		0.0	Lung ca. (small cell)	LX-1	3.1
Brain (hippocampus)		0.0	Lung ca. (small cell)	NCI-H69	0.2
Brain (substantia nigra)		0.0	Lung ca. (s.cell var.)	SHP-77	0.0
Brain (thalamus)		0.0	Lung ca. (large cell)	NCI-H460	0.0
Brain (hypothalamus)		0.0	Lung ca. (non-sm. cell)	A549	2.2
Spinal cord		0.0	Lung ca. (non-s.cell)	NCI-H23	0.0
CNS ca. (glio/astro)	U87-MG	0.0	Lung ca (non-s.cell)	HOP-62	0.0
CNS ca. (glio/astro)	U-118-MG	0.0	Lung ca. (non-s.cl)	NCI-H522	0.0
CNS ca. (astro)	SW1783	0.3	Lung ca. (squam.)	SW 900	0.6
CNS ca.* (neuro; met)	SK-N-AS	6.7	Lung ca. (squam.)	NCI-H596	0.2
CNS ca. (astro)	SF-539	0.0	Mammary gland		0.0
CNS ca. (astro)	SNB-75	0.0	Breast ca.* (pl. effusion)	MCF-7	0.0
CNS ca. (glio)	SNB-19	0.0	Breast ca.* (pl.ef)	MDA-MB-231	0.0
CNS ca. (glio)	U251	0.6	Breast ca.* (pl. effusion)	T47D	0.0
CNS ca. (glio)	SF-295	15.3	Breast ca.	BT-549	0.0
Heart		0.0	Breast ca.	MDA-N	0.0
Skeletal muscle		0.0	Ovary		0.0
Bone marrow		0.0	Ovarian ca.	OVCAR-3	0.0
Thymus		0.0	Ovarian ca.	OVCAR-4	0.0
Spleen		0.0	Ovarian ca.	OVCAR-5	0.1
Lymph node		0.0	Ovarian ca.	OVCAR-8	0.0
Colon (ascending)		0.0	Ovarian ca.	IGROV-1	0.0
Stomach		0.0	Ovarian ca.* (ascites)	SK-OV-3	0.0
Small intestine		0.0	Uterus		7.4
Colon ca.	SW480	2.4	Placenta		100.0
Colon ca.* (SW480		4.1	Prostate		0.0

met)SW620

Colon ca.	HT29	0.0	Prostate ca.* (bone met)PC-3	0.0
Colon ca.	HCT-116	0.0	Testis	4.2
Colon ca.	CaCo-2	0.0	Melanoma Hs688(A).T	0.0
Colon ca.	HCT-15	0.0	Melanoma* (met) Hs688(B).T	0.0
Colon ca.	HCC-2998	0.0	Melanoma UACC-62	0.0
Gastric ca.* (liver met) NCI-N87		45.4	Melanoma M14	0.0
Bladder		0.0	Melanoma LOX IMVI	0.0
Trachea		0.0	Melanoma* (met) SK-MEL-5	0.0
Kidney		4.1	Melanoma SK-MEL-28	0.0

Table AA. Panel 4D

Tissue Name

	Rel. Expr., % 4dx4tm5043f_ ag217_b1	Rel. Expr., % 4dx4tm5056f_ ag217_b1
93768_Secondary Th1_anti-CD28/anti-CD3	0.0	1.2
93769_Secondary Th2_anti-CD28/anti-CD3	0.0	0.0
93770_Secondary Tr1_anti-CD28/anti-CD3	2.6	0.0
93573_Secondary Th1_resting day 4-6 in IL-2	1.8	0.0
93572_Secondary Th2_resting day 4-6 in IL-2	0.0	0.0
93571_Secondary Tr1_resting day 4-6 in IL-2	7.0	1.6
93568_primary Th1_anti-CD28/anti-CD3	0.0	0.0
93569_primary Th2_anti-CD28/anti-CD3	0.0	0.0
93570_primary Tr1_anti-CD28/anti-CD3	0.8	0.0
93565_primary Th1_resting dy 4-6 in IL-2	0.0	0.0
93566_primary Th2_resting dy 4-6 in IL-2	0.0	0.0
93567_primary Tr1_resting dy 4-6 in IL-2	0.0	1.3
93351_CD45RA CD4 lymphocyte_anti-CD28/anti-CD3	8.1	9.2
93352_CD45RO CD4 lymphocyte_anti-CD28/anti-CD3	0.0	0.0
93251_CD8 Lymphocytes_anti-CD28/anti-CD3	0.0	0.0
93353_chronic CD8 Lymphocytes 2ry_resting dy 4-6 in IL-2	0.0	0.0
93574_chronic CD8 Lymphocytes 2ry_activated CD3/CD28	2.1	2.5
93354_CD4_none	0.0	0.0
93252_Secondary Th1/Th2/Tr1_anti-CD95 CH11	0.0	0.0
93103_LAK cells_resting	0.0	0.0
93788_LAK cells_IL-2	0.0	0.0
93787_LAK cells_IL-2+IL-12	0.0	0.0
93789_LAK cells_IL-2+IFN gamma	0.0	0.0
93790_LAK cells_IL-2+ IL-18	2.2	0.0
93104_LAK cells_PMA/ionomycin and IL-18	0.0	0.0
93578_NK Cells IL-2_resting	0.0	0.0
93109_Mixed Lymphocyte Reaction_Two Way MLR	0.0	0.0

WO 01/90155	PCT/US01/17073	
93110_Mixed Lymphocyte Reaction_Two Way MLR	0.0	0.0
93111_Mixed Lymphocyte Reaction_Two Way MLR	0.0	1.5
93112_Mononuclear Cells (PBMCs)_resting	0.0	0.0
93113_Mononuclear Cells (PBMCs)_PWM	0.0	0.0
93114_Mononuclear Cells (PBMCs)_PHA-L	0.0	0.0
93249_Ramos (B cell)_none	0.0	0.0
93250_Ramos (B cell)_ionomycin	0.0	1.5
93349_B lymphocytes_PWM	0.0	3.4
93350_B lymphocytes_CD40L and IL-4	0.0	1.7
92665_EOL-1 (Eosinophil)_dbcAMP differentiated	0.0	0.0
93248_EOL-1 (Eosinophil)_dbcAMP/PMAionomycin	0.0	0.0
93356_Dendritic Cells_none	0.0	0.0
93355_Dendritic Cells_LPS 100 ng/ml	1.9	1.4
93775_Dendritic Cells_anti-CD40	0.0	0.0
93774_Monocytes_resting	0.0	0.0
93776_Monocytes_LPS 50 ng/ml	0.0	0.0
93581_Macrophages_resting	0.0	1.5
93582_Macrophages_LPS 100 ng/ml	6.4	0.0
93098_HUVEC (Endothelial)_none	0.0	0.0
93099_HUVEC (Endothelial)_starved	0.0	0.0
93100_HUVEC (Endothelial)_IL-1b	0.0	0.0
93779_HUVEC (Endothelial)_IFN gamma	0.0	0.0
93102_HUVEC (Endothelial)_TNF alpha + IFN gamma	0.0	0.0
93101_HUVEC (Endothelial)_TNF alpha + IL4	0.0	0.0
93781_HUVEC (Endothelial)_IL-11	0.0	2.8
93583_Lung Microvascular Endothelial Cells_none	0.0	1.1
93584_Lung Microvascular Endothelial Cells_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0.0	0.0
92662_Microvascular Dermal endothelium_none	3.7	0.0
92663_Microvascular Dermal endothelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0.0	0.0
93773_Bronchial epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml) **	3.9	3.2
93347_Small Airway Epithelium_none	6.2	4.5
93348_Small Airway Epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	11.2	9.7
92668_Coronary Artery SMC_resting	5.8	5.9
92669_Coronary Artery SMC_TNFa (4 ng/ml) and IL1b (1 ng/ml)	4.2	1.9
93107_astrocytes_resting	61.1	41.5
93108_astrocytes_TNFa (4 ng/ml) and IL1b (1 ng/ml)	78.6	69.9
92666_KU-812 (Basophil)_resting	0.0	0.0
92667_KU-812 (Basophil)_PMA/ionomycin	0.0	0.0
93579_CCD1106 (Keratinocytes)_none	0.0	0.0

WO 01/90155	PCT/US01/17073	
93580_CCD1106 (Keratinocytes)_TNFa and IFNg **	0.0	0.0
93791_Liver Cirrhosis	10.9	5.4
93792_Lupus Kidney	0.0	2.3
93577_NCI-H292	11.6	2.8
93358_NCI-H292_IL-4	2.9	3.3
93360_NCI-H292_IL-9	2.3	1.8
93359_NCI-H292_IL-13	2.8	0.0
93357_NCI-H292_IFN gamma	3.8	0.0
93777_HPAEC_-	0.0	0.0
93778_HPAEC_IL-1 beta/TNA alpha	0.0	0.0
93254_Normal Human Lung Fibroblast_none	0.0	0.0
93253_Normal Human Lung Fibroblast_TNFa (4 ng/ml) and IL-1b (1 ng/ml)	0.0	0.0
93257_Normal Human Lung Fibroblast_IL-4	0.0	0.0
93256_Normal Human Lung Fibroblast_IL-9	0.0	0.0
93255_Normal Human Lung Fibroblast_IL-13	0.0	0.0
93258_Normal Human Lung Fibroblast_IFN gamma	0.0	1.3
93106_Dermal Fibroblasts CCD1070_resting	40.7	30.0
93361_Dermal Fibroblasts CCD1070_TNF alpha 4 ng/ml	13.1	17.9
93105_Dermal Fibroblasts CCD1070_IL-1 beta 1 ng/ml	27.0	19.2
93772_dermal fibroblast_IFN gamma	0.0	0.0
93771_dermal fibroblast_IL-4	2.3	2.6
93259_IBD Colitis 1**	0.0	0.0
93260_IBD Colitis 2	2.3	0.0
93261_IBD Crohns	0.0	1.1
735010_Colon_normal	18.6	5.9
735019_Lung_none	13.2	8.1
64028-1_Thymus_none	100.0	100.0
64030-1_Kidney_none	3.9	1.6

Panel 1 Summary: Expression of NOV8c is highest in the placenta, followed by the uterus, testis and kidney. Interestingly, expression in adult kidney is considerably higher than in fetal kidney. Among disease tissues, strong expression is seen in gastric cancer, with lower levels in lung, colon, CNS, ovarian and pancreatic cancers. This pattern indicates that this gene may be a therapeutic target in these conditions.

Panel 4D Summary: This transcript is highly expressed in the thymus and astrocytes, with lower levels of this transcript are seen in colon and lung, as well as in dermal fibroblasts (either resting or IL-1-treated or TNF-treated). Thymus expression of the transcript suggests that it may be important in T cell development. Retinoic acid has been shown to have effects on T cell development. Agonistic or antagonistic therapies directed against the protein encoded for

by this transcript could be used for immune regulation during organ engraftment or as treatment for T cell cancers. [Reference: Yagi J. et al., Cell Immunol 1997 Nov 1;181(2):153-62.

Influence of retinoic acid on the differentiation pathway of T cells in the thymus. This study investigated the ability of retinoic acid (RA) to influence T cell differentiation. All-trans-RA had marked effects on T cell differentiation in murine fetal thymic organ cultures (FTOCs). The time course of the effect of all-trans-RA in FTOC of day 14 C57BL/6 embryos revealed a twofold increase in the frequency of CD4 single-positive (SP) cells and a high level of CD3-bearing cells (CD3^{high} cells) at a later stage of T cell development. At an earlier stage, all-trans-RA induced a twofold increase in the frequency of CD4 SP cells, but significantly suppressed the upregulation of CD3 and TCR. Reverse transcription-PCR using RA receptor (RAR) subtype-specific primers showed that RAR alpha but not beta and gamma is expressed during T cell development in the thymus and that its expression was associated with the generation of CD4/CD8 double-positive (DP) cells. In FTOC of day 16 BALB/c embryos, the level of V beta 3^{high} cells was greatly reduced (1.4% of the CD3^{high} cells) in response to the mouse mammary tumor virus-6-encoded superantigen, but V beta 3-bearing cells were rescued from the deletion in the presence of all-trans-RA (5.6% of the CD3^{high} cells). Further, the inhibitory effect of all-trans-RA on thymocyte deletion was observed when the deletion was induced by a low concentration of staphylococcal enterotoxin B in FTOC. Taken together, these data suggest that RA increases the frequency of mature and self-reactive T cells in the thymus, possibly by inhibiting the process of negative selection at the DP stage of T cell differentiation.]

NOV9

Expression of gene NOV9 was assessed using the primer-probe Ag1249, described in Table BB. Results of the RTQ-PCR runs are shown in Table CC and DD.

Table BB. Probe Name: Ag1249

Primers	Sequences	TM	Length	Start Position
Forward	5'-CAAATGAAGGAGCATGAGAAAG-3' (SEQ ID NO:98)	59	22	76
Probe	FAM-5'-CCCTGAAATGCTAACTGATCTCCAATG-3'-TAMRA (SEQ ID NO:99)	66.8	27	99
Reverse	5'-TGGGATACTTGTCATAGGACTTG-3' (SEQ ID NO:100)	59.1	22	135

Table CC. Panel 1.2

Tissue Name	Rel. Expr., % 1.2tm1420f_ag 1249	Tissue Name	Rel. Expr., % 1.2tm1420f_ag 1249
Endothelial cells	0.0	Kidney (fetal)	0.0
Endothelial cells (treated)	0.0	Renal ca. 786-0	0.0
Pancreas	0.0	Renal ca. A498	0.0
Pancreatic ca. CAPAN 2	0.0	Renal ca. RXF 393	0.0
Adrenal Gland (new lot*)	0.0	Renal ca. ACHN	0.0
Thyroid	0.0	Renal ca. UO-31	0.0
Salivary gland	0.0	Renal ca. TK-10	0.0
Pituitary gland	0.0	Liver	0.0
Brain (fetal)	0.0	Liver (fetal)	0.0
Brain (whole)	0.0	Liver ca. (hepatoblast) HepG2	0.0
Brain (amygdala)	0.0	Lung	0.0
Brain (cerebellum)	0.0	Lung (fetal)	0.0
Brain (hippocampus)	0.0	Lung ca. (small cell) LX-1	0.0
Brain (thalamus)	0.0	Lung ca. (small cell) NCI-H69	0.0
Cerebral Cortex	0.0	Lung ca. (s.cell var.) SHP-77	0.0
Spinal cord	0.0	Lung ca. (large cell) NCI-H460	0.0
CNS ca. (glio/astro) U87-MG	0.0	Lung ca. (non-sm. cell) A549	0.0
CNS ca. (glio/astro) U-118-MG	0.0	Lung ca. (non-s.cell) NCI-H23	0.0
CNS ca. (astro) SW1783	0.0	Lung ca (non-s.cell) HOP-62	0.0
CNS ca.* (neuro; met) SK-N-AS	0.0	Lung ca. (non-s.cl) NCI-H522	0.0
CNS ca. (astro) SF-539	0.0	Lung ca. (squam.) SW 900	0.0
CNS ca. (astro) SNB-75	0.0	Lung ca. (squam.) NCI-H596	0.0
CNS ca. (glio) SNB-19	0.0	Mammary gland	0.0
CNS ca. (glio) U251	0.0	Breast ca.* (pl. effusion) MCF-7	0.0
CNS ca. (glio) SF-295	0.0	Breast ca.* (pl.ef) MDA-MB-231	0.0
Heart	0.0	Breast ca.* (pl. effusion) T47D	0.0
Skeletal Muscle (new lot*)	0.0	Breast ca. BT-549	0.0
Bone marrow	0.0	Breast ca. MDA-N	0.0
Thymus	0.0	Ovary	0.0
Spleen	0.0	Ovarian ca. OVCAR-3	0.0
Lymph node	0.0	Ovarian ca. OVCAR-4	0.0
Colorectal	0.0	Ovarian ca. OVCAR-5	0.0
Stomach	0.0	Ovarian ca. OVCAR-8	0.0

Small intestine	0.0	Ovarian ca.	IGROV-1	0.0
Colon ca. SW480	0.0	Ovarian ca.* (ascites)	SK-OV-3	11.7
Colon ca.* (SW480 met)SW620	0.0	Uterus		0.0
Colon ca. HT29	0.0	Placenta		0.0
Colon ca. HCT-116	0.0	Prostate		0.0
Colon ca. CaCo-2	0.0	Prostate ca.* (bone met)PC-3		0.0
83219 CC Well to Mod Diff (ODO3866)	0.0	Testis		0.0
Colon ca. HCC-2998	0.0	Melanoma Hs688(A).T		0.0
Gastric ca.* (liver met) NCI-N87	0.0	Melanoma* (met) Hs688(B).T		0.0
Bladder	0.0	Melanoma UACC-62		0.0
Trachea	0.0	Melanoma M14		0.0
Kidney	0.0	Melanoma LOX IMVI		0.0

Table DD. Panel 4D

Tissue Name	Rel. Expr., % 4Dtm2108f_ag1249	Rel. Expr., % 4Dtm2161f_ag1249
93768_Secondary Th1_anti-CD28/anti-CD3	0.0	0.0
93769_Secondary Th2_anti-CD28/anti-CD3	0.0	0.0
93770_Secondary Tr1_anti-CD28/anti-CD3	0.0	0.0
93573_Secondary Th1_resting day 4-6 in IL-2	0.1	0.0
93572_Secondary Th2_resting day 4-6 in IL-2	0.0	0.0
93571_Secondary Tr1_resting day 4-6 in IL-2	0.2	0.0
93568_primary Th1_anti-CD28/anti-CD3	0.0	3.6
93569_primary Th2_anti-CD28/anti-CD3	0.0	0.0
93570_primary Tr1_anti-CD28/anti-CD3	0.0	0.0
93565_primary Th1_resting dy 4-6 in IL-2	0.0	0.0
93566_primary Th2_resting dy 4-6 in IL-2	0.0	0.0
93567_primary Tr1_resting dy 4-6 in IL-2	100.0	0.0
93351_CD45RA CD4 lymphocyte_anti-CD28/anti-CD3	0.0	0.0
93352_CD45RO CD4 lymphocyte_anti-CD28/anti-CD3	0.0	0.0
93251_CD8 Lymphocytes_anti-CD28/anti-CD3	0.0	0.0
93353_chronic CD8 Lymphocytes 2ry_resting dy 4-6 in IL-2	0.0	0.0
93574_chronic CD8 Lymphocytes 2ry_activated CD3/CD28	0.0	0.0
93354_CD4_none	0.0	0.0
93252_Secondary Th1/Th2/Tr1_anti-CD95 CH11	0.0	0.0
93103_LAK cells_resting	0.0	0.0
93788_LAK cells_IL-2	0.0	0.0
93787_LAK cells_IL-2+IL-12	0.0	0.0

93789_LAK cells_IL-2+IFN gamma	0.0	0.0
93790_LAK cells_IL-2+ IL-18	0.0	0.0
93104_LAK cells_PMA/ionomycin and IL-18	0.0	0.0
93578_NK Cells IL-2_resting	0.0	0.0
93109_Mixed Lymphocyte Reaction_Two Way MLR	0.0	0.0
93110_Mixed Lymphocyte Reaction_Two Way MLR	0.8	0.0
93111_Mixed Lymphocyte Reaction_Two Way MLR	0.0	0.0
93112_Mononuclear Cells (PBMCs)_resting	0.0	0.0
93113_Mononuclear Cells (PBMCs)_PWM	0.0	0.0
93114_Mononuclear Cells (PBMCs)_PHA-L	0.0	0.0
93249_Ramos (B cell)_none	0.0	0.0
93250_Ramos (B cell)_ionomycin	0.0	0.0
93349_B lymphocytes_PWM	0.0	0.0
93350_B lymphocytes_CD40L and IL-4	0.0	0.0
92665_EOL-1 (Eosinophil)_dbcAMP differentiated	0.0	0.0
93248_EOL-1 (Eosinophil)_dbcAMP/PMAionomycin	0.0	0.0
93356_Dendritic Cells_none	0.0	0.0
93355_Dendritic Cells_LPS 100 ng/ml	0.0	0.0
93775_Dendritic Cells_anti-CD40	0.0	0.0
93774_Monocytes_resting	0.0	0.0
93776_Monocytes_LPS 50 ng/ml	0.0	0.0
93581_Macrophages_resting	0.0	0.0
93582_Macrophages_LPS 100 ng/ml	0.0	0.0
93098_HUVEC (Endothelial)_none	0.0	0.0
93099_HUVEC (Endothelial)_starved	0.0	0.0
93100_HUVEC (Endothelial)_IL-1b	0.0	0.0
93779_HUVEC (Endothelial)_IFN gamma	0.0	0.0
93102_HUVEC (Endothelial)_TNF alpha + IFN gamma	0.0	0.0
93101_HUVEC (Endothelial)_TNF alpha + IL4	0.0	0.0
93781_HUVEC (Endothelial)_IL-11	0.0	0.0
93583_Lung Microvascular Endothelial Cells_none	0.0	9.5
93584_Lung Microvascular Endothelial Cells_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0.0	0.0
92662_Microvascular Dermal endothelium_none	0.0	0.0
92663_Microvascular Dermal endothelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0.0	0.0
93773_Bronchial epithelium_TNFa (4 ng/ml)	0.0	6.6

and IL1b (1 ng/ml) **

93347_Small Airway Epithelium_none	0.0	0.0
93348_Small Airway Epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0.6	0.0
92668_Coronary Artery SMC_resting	0.0	0.0
92669_Coronary Artery SMC_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0.0	0.0
93107_astrocytes_resting	0.0	0.0
93108_astrocytes_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0.0	0.0
92666_KU-812 (Basophil)_resting	0.0	0.0
92667_KU-812 (Basophil)_PMA/ionoycin	0.0	0.0
93579_CCD1106 (Keratinocytes)_none	1.3	0.0
93580_CCD1106 (Keratinocytes)_TNFa and IFNg **	0.6	18.0
93791_Liver Cirrhosis	4.4	20.0
93792_Lupus Kidney	0.6	0.0
93577_NCI-H292	0.0	0.0
93358_NCI-H292_IL-4	0.0	0.0
93360_NCI-H292_IL-9	0.0	0.0
93359_NCI-H292_IL-13	0.0	8.0
93357_NCI-H292_IFN gamma	0.0	0.0
93777_HPAEC_-	0.0	0.0
93778_HPAEC_IL-1 beta/TNA alpha	0.0	0.0
93254_Normal Human Lung Fibroblast_none	0.0	0.0
93253_Normal Human Lung Fibroblast_TNFa (4 ng/ml) and IL-1b (1 ng/ml)	0.0	0.0
93257_Normal Human Lung Fibroblast_IL-4	0.0	0.0
93256_Normal Human Lung Fibroblast_IL-9	0.0	0.0
93255_Normal Human Lung Fibroblast_IL-13	0.0	0.0
93258_Normal Human Lung Fibroblast_IFN gamma	0.0	0.0
93106_Dermal Fibroblasts CCD1070_resting	0.0	0.0
93361_Dermal Fibroblasts CCD1070_TNF alpha 4 ng/ml	0.0	0.0
93105_Dermal Fibroblasts CCD1070_IL-1 beta 1 ng/ml	1.0	0.0
93772_dermal fibroblast_IFN gamma	0.0	0.0
93771_dermal fibroblast_IL-4	0.0	0.0
93259_IBD Colitis 1**	10.6	100.0
93260_IBD Colitis 2	2.2	5.9
93261_IBD Crohns	0.7	0.0
735010_Colon_normal	0.7	0.0
735019_Lung_none	0.0	0.0
64028-1_Thymus_none	1.6	0.0

Panel 1.2 Summary: Highest expression of NOV9 is in a sample of adipose tissue, which is known to be contaminated with genomic DNA. The only other sample that shows evidence of expression of this gene was derived from a metastatic ovarian cancer cells line that grew as an ascites. This type of tumor growth, as a liquid cell suspension in a body cavity, is quite unique. The expression of this gene may portend to this type of growth and thus, therapeutic targeting of this gene may have therapeutic benefit for ascites growth.

Panel 4D Summary: Run 2108 does not show a good amplification plot and is therefore not being considered for this analysis. Run 2161 shows highest expression in the colitis 1 sample, probably due to genomic DNA contamination. Levels in other samples are below the detectable level.

OTHER EMBODIMENTS

Although particular embodiments have been disclosed herein in detail, this has been done by way of example for purposes of illustration only, and is not intended to be limiting with respect to the scope of the appended claims, which follow. In particular, it is contemplated by the inventors that various substitutions, alterations, and modifications may be made to the invention without departing from the spirit and scope of the invention as defined by the claims. The choice of nucleic acid starting material, clone of interest, or library type is believed to be a matter of routine for a person of ordinary skill in the art with knowledge of the embodiments described herein. Other aspects, advantages, and modifications considered to be within the scope of the following claims.

WHAT IS CLAIMED IS:

1. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of:
 - (a) a mature form of an amino acid sequence selected from the group consisting of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, and 34;
 - (b) a variant of a mature form of an amino acid sequence selected from the group consisting of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, and 34, wherein one or more amino acid residues in said variant differs from the amino acid sequence of said mature form, provided that said variant differs in no more than 15% of the amino acid residues from the amino acid sequence of said mature form;
 - (c) an amino acid sequence selected from the group consisting SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, and 34; and
 - (d) a variant of an amino acid sequence selected from the group consisting of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, and 34, wherein one or more amino acid residues in said variant differs from the amino acid sequence of said mature form, provided that said variant differs in no more than 15% of amino acid residues from said amino acid sequence.
2. The polypeptide of claim 1, wherein said polypeptide comprises the amino acid sequence of a naturally-occurring allelic variant of an amino acid sequence selected from the group consisting SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, and 34.
3. The polypeptide of claim 2, wherein said allelic variant comprises an amino acid sequence that is the translation of a nucleic acid sequence differing by a single nucleotide from a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, and 33.
4. The polypeptide of claim 1, wherein the amino acid sequence of said variant comprises a conservative amino acid substitution.

5. An isolated nucleic acid molecule comprising a nucleic acid sequence encoding a polypeptide comprising an amino acid sequence selected from the group consisting of:
 - (a) a mature form of an amino acid sequence selected from the group consisting of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, and 34;
 - (b) a variant of a mature form of an amino acid sequence selected from the group consisting of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, and 35, wherein one or more amino acid residues in said variant differs from the amino acid sequence of said mature form, provided that said variant differs in no more than 15% of the amino acid residues from the amino acid sequence of said mature form;
 - (c) an amino acid sequence selected from the group consisting of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, and 34;
 - (d) a variant of an amino acid sequence selected from the group consisting SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, and 34, wherein one or more amino acid residues in said variant differs from the amino acid sequence of said mature form, provided that said variant differs in no more than 15% of amino acid residues from said amino acid sequence;
 - (e) a nucleic acid fragment encoding at least a portion of a polypeptide comprising an amino acid sequence chosen from the group consisting of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, and 34, or a variant of said polypeptide, wherein one or more amino acid residues in said variant differs from the amino acid sequence of said mature form, provided that said variant differs in no more than 15% of amino acid residues from said amino acid sequence; and
 - (f) a nucleic acid molecule comprising the complement of (a), (b), (c), (d) or (e).
6. The nucleic acid molecule of claim 5, wherein the nucleic acid molecule comprises the nucleotide sequence of a naturally-occurring allelic nucleic acid variant.
7. The nucleic acid molecule of claim 5, wherein the nucleic acid molecule encodes a polypeptide comprising the amino acid sequence of a naturally-occurring polypeptide variant.

8. The nucleic acid molecule of claim 5, wherein the nucleic acid molecule differs by a single nucleotide from a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, and 33.
9. The nucleic acid molecule of claim 5, wherein said nucleic acid molecule comprises a nucleotide sequence selected from the group consisting of:
 - (a) a nucleotide sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, and 33;
 - (b) a nucleotide sequence differing by one or more nucleotides from a nucleotide sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, and 33, provided that no more than 20% of the nucleotides differ from said nucleotide sequence;
 - (c) a nucleic acid fragment of (a); and
 - (d) a nucleic acid fragment of (b).
10. The nucleic acid molecule of claim 5, wherein said nucleic acid molecule hybridizes under stringent conditions to a nucleotide sequence chosen from the group consisting of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, and 33, or a complement of said nucleotide sequence.
11. The nucleic acid molecule of claim 5, wherein the nucleic acid molecule comprises a nucleotide sequence selected from the group consisting of:
 - (a) a first nucleotide sequence comprising a coding sequence differing by one or more nucleotide sequences from a coding sequence encoding said amino acid sequence, provided that no more than 20% of the nucleotides in the coding sequence in said first nucleotide sequence differ from said coding sequence;
 - (b) an isolated second polynucleotide that is a complement of the first polynucleotide; and
 - (c) a nucleic acid fragment of (a) or (b).
12. A vector comprising the nucleic acid molecule of claim 11.

13. The vector of claim 12, further comprising a promoter operably-linked to said nucleic acid molecule.
14. A cell comprising the vector of claim 12.
15. An antibody that binds immunospecifically to the polypeptide of claim 1.
16. The antibody of claim 15, wherein said antibody is a monoclonal antibody.
17. The antibody of claim 15, wherein the antibody is a humanized antibody.
18. A method for determining the presence or amount of the polypeptide of claim 1 in a sample, the method comprising:
 - (a) providing the sample;
 - (b) contacting the sample with an antibody that binds immunospecifically to the polypeptide; and
 - (c) determining the presence or amount of antibody bound to said polypeptide,thereby determining the presence or amount of polypeptide in said sample.
19. A method for determining the presence or amount of the nucleic acid molecule of claim 5 in a sample, the method comprising:
 - (a) providing the sample;
 - (b) contacting the sample with a probe that binds to said nucleic acid molecule; and
 - (c) determining the presence or amount of the probe bound to said nucleic acid molecule,thereby determining the presence or amount of the nucleic acid molecule in said sample.
20. The method of claim 19 wherein presence or amount of the nucleic acid molecule is used as a marker for cell or tissue type.
21. The method of claim 20 wherein the cell or tissue type is cancerous.

22. A method of identifying an agent that binds to a polypeptide of claim 1, the method comprising:
- (a) contacting said polypeptide with said agent; and
 - (b) determining whether said agent binds to said polypeptide.
23. The method of claim 22 wherein the agent is a cellular receptor or a downstream effector.
24. A method for identifying an agent that modulates the expression or activity of the polypeptide of claim 1, the method comprising:
- (a) providing a cell expressing said polypeptide;
 - (b) contacting the cell with said agent, and
 - (c) determining whether the agent modulates expression or activity of said polypeptide,
- whereby an alteration in expression or activity of said peptide indicates said agent modulates expression or activity of said polypeptide.
25. A method for modulating the activity of the polypeptide of claim 1, the method comprising contacting a cell sample expressing the polypeptide of said claim with a compound that binds to said polypeptide in an amount sufficient to modulate the activity of the polypeptide.
26. A method of treating or preventing a NOVX-associated disorder, said method comprising administering to a subject in which such treatment or prevention is desired the polypeptide of claim 1 in an amount sufficient to treat or prevent said NOVX-associated disorder in said subject.
27. The method of claim 26 wherein the disorder is selected from the group consisting of cardiomyopathy and atherosclerosis.
28. The method of claim 26 wherein the disorder is related to cell signal processing and metabolic pathway modulation.

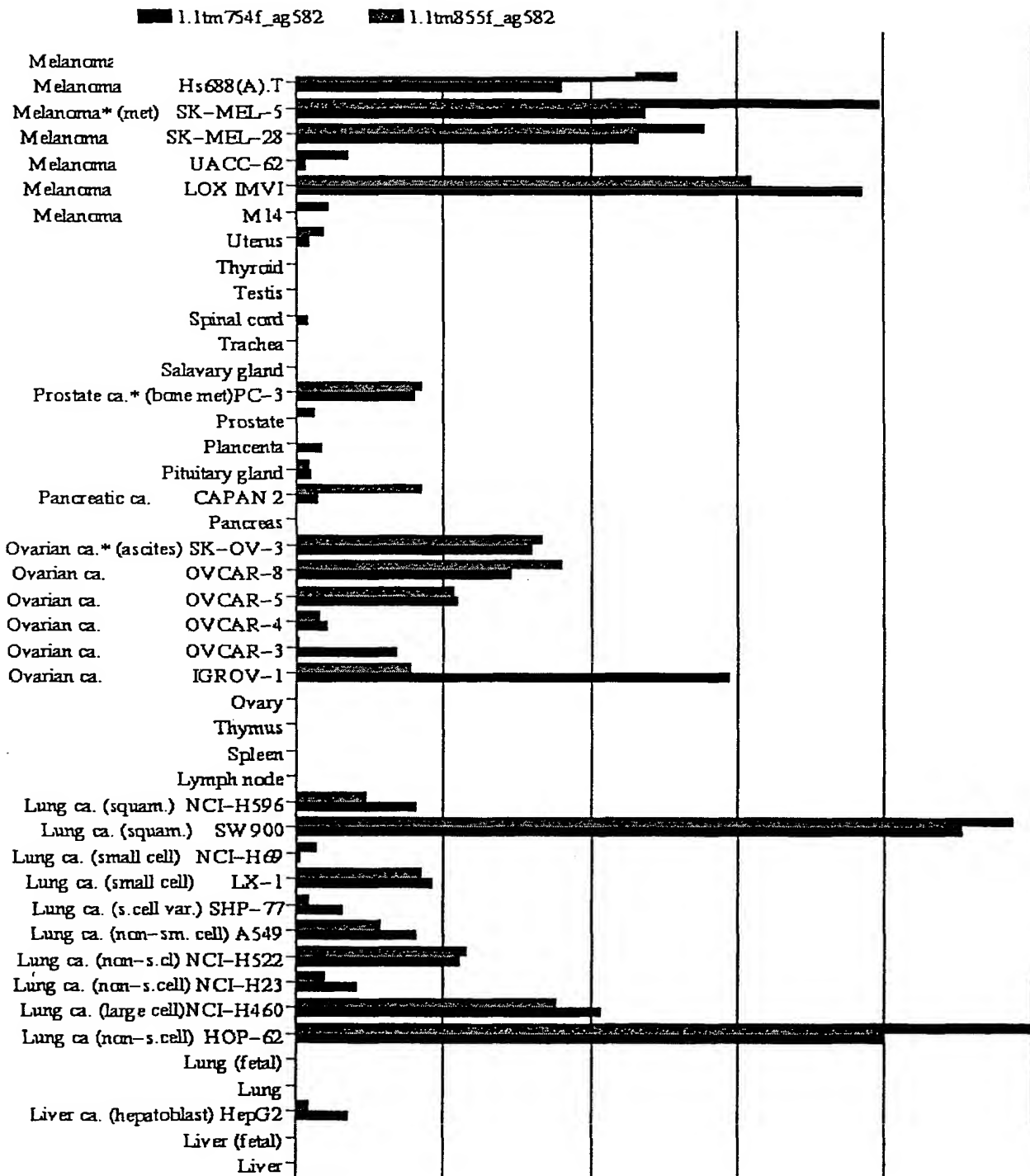
29. The method of claim 26, wherein said subject is a human.
30. A method of treating or preventing a NOVX-associated disorder, said method comprising administering to a subject in which such treatment or prevention is desired the nucleic acid of claim 5 in an amount sufficient to treat or prevent said NOVX-associated disorder in said subject.
31. The method of claim 30 wherein the disorder is selected from the group consisting of cardiomyopathy and atherosclerosis.
32. The method of claim 30 wherein the disorder is related to cell signal processing and metabolic pathway modulation.
33. The method of claim 30, wherein said subject is a human.
34. A method of treating or preventing a NOVX-associated disorder, said method comprising administering to a subject in which such treatment or prevention is desired the antibody of claim 15 in an amount sufficient to treat or prevent said NOVX-associated disorder in said subject.
35. The method of claim 34 wherein the disorder is diabetes.
36. The method of claim 34 wherein the disorder is related to cell signal processing and metabolic pathway modulation.
37. The method of claim 34, wherein the subject is a human.
38. A pharmaceutical composition comprising the polypeptide of claim 1 and a pharmaceutically-acceptable carrier.
39. A pharmaceutical composition comprising the nucleic acid molecule of claim 5 and a pharmaceutically-acceptable carrier.

40. A pharmaceutical composition comprising the antibody of claim 15 and a pharmaceutically-acceptable carrier.
41. A kit comprising in one or more containers, the pharmaceutical composition of claim 38.
42. A kit comprising in one or more containers, the pharmaceutical composition of claim 39.
43. A kit comprising in one or more containers, the pharmaceutical composition of claim 40.
44. A method for determining the presence of or predisposition to a disease associated with altered levels of the polypeptide of claim 1 in a first mammalian subject, the method comprising:
- (a) measuring the level of expression of the polypeptide in a sample from the first mammalian subject; and
 - (b) comparing the amount of said polypeptide in the sample of step (a) to the amount of the polypeptide present in a control sample from a second mammalian subject known not to have, or not to be predisposed to, said disease;
- wherein an alteration in the expression level of the polypeptide in the first subject as compared to the control sample indicates the presence of or predisposition to said disease.
45. The method of claim 44 wherein the predisposition is to cancers.
46. A method for determining the presence of or predisposition to a disease associated with altered levels of the nucleic acid molecule of claim 5 in a first mammalian subject, the method comprising:
- (a) measuring the amount of the nucleic acid in a sample from the first mammalian subject; and
 - (b) comparing the amount of said nucleic acid in the sample of step (a) to the amount of the nucleic acid present in a control sample from a second mammalian subject known not to have or not be predisposed to, the disease;

wherein an alteration in the level of the nucleic acid in the first subject as compared to the control sample indicates the presence of or predisposition to the disease.

47. The method of claim 46 wherein the predisposition is to a cancer.
48. A method of treating a pathological state in a mammal, the method comprising administering to the mammal a polypeptide in an amount that is sufficient to alleviate the pathological state, wherein the polypeptide is a polypeptide having an amino acid sequence at least 95% identical to a polypeptide comprising an amino acid sequence of at least one of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, and 34, or a biologically active fragment thereof.
49. A method of treating a pathological state in a mammal, the method comprising administering to the mammal the antibody of claim 15 in an amount sufficient to alleviate the pathological state.

Figure 1.



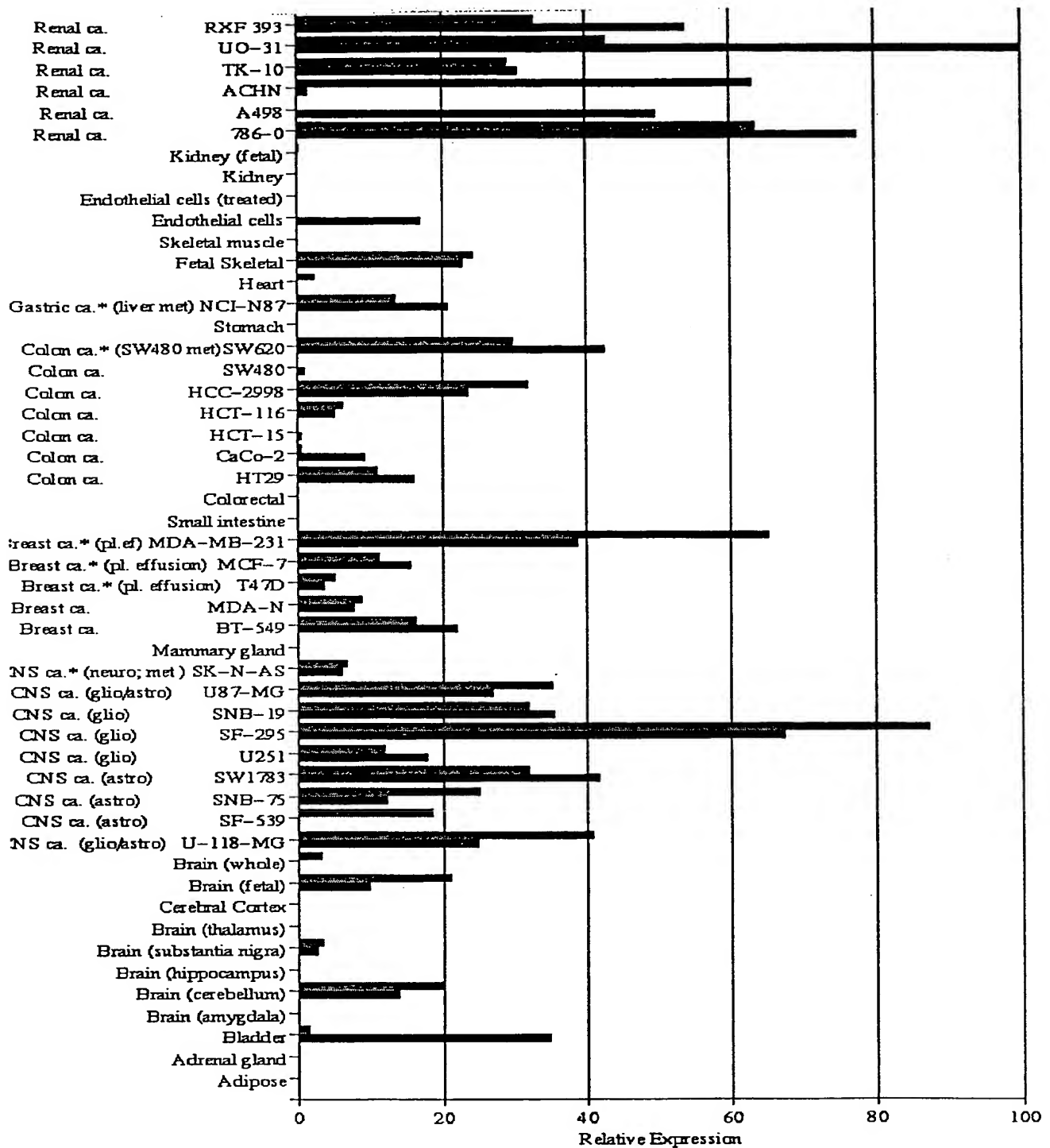


Figure 2.

